

SEQUENCE LISTING

<110> Diversa Corporation
 Kerovuo, Janne
 Solbak, Arne
 Gray, Kevin
 McCann, Ryan
 Purohit, Shalaka
 Gerendash, Joel
 Janssen, Giselle
 Dahod, Samun

<120> PECTATE LYASES, NUCLEIC ACIDS ENCODING
 THEM AND METHODS FOR MAKING AND USING THEM

<130> 564462009640

<140> To Be Assigned

<141> Concurrently herewith

<150> 60/460,842

<151> 2003-04-04

<150> 60/484,798

<151> 2003-07-03

<160> 134

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1917

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 1

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acaattcaac	aagcgggtga	ccagggtccc	aaagacaata	cacacccggt	cttgattcag	180
atcaaaccgg	gtgtgtatca	ggaacagggt	cgtgtcgccg	ccggcaaacg	ctttatcact	240
tttcgcgggc	acgatgcgag	caagaccgtc	atcacctatc	gattgagcgc	actgcaagcg	300
ggaaataccc	ggctggcatt	caccaccttc	gttaatgcag	acgactttcg	cgccgagaa	360
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gaccgcgcga	cgtttgaaaa	ctgccgggtc	ctcggttggc	aggacacttt	gtttgtgaac	480
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acggcctccg	ccgtgtttga	gaactgcacc	attcacagca	aaggcgaagg	ttatgtgacc	600
gcacactatc	gcaccagcga	tgagatggat	accggttttg	tctttcatcg	ttgtcgtttg	660
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gctaataccc	tagctcgtgt	cgcgtgggtc	aggcagttga	cgacagaaca	agccgccgag	900
ttttcgcggg	aacgcttttt	cagccgcgct	gttcgcgggc	tctctgggca	ggccaaccag	960
gcagtcggaa	cgatcgcgtg	ggacgatgcy	cagaaaaaac	cgaacgagtg	gtatgcgagc	1020
gccgaggcgt	tgcgcattgc	cgacaacgtt	gttctttatc	aacgtgactc	cggcggttgg	1080
cccaagaaca	tcgacatggg	gaagccgctc	gacgaaaagg	gtcgaagccg	tcttctgcgc	1140

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gtgcgtaaga agaacgattc cacgatcgac aatggcgcgga cttacacgca actctcgttt 1200
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ctcgattacc tgttgaaggc gcagtatcca aacggaggct ggccgcagtt ctatccaac 1320
ctcaacggct attacaaaca catcactttc aacgacaacg ccatgatcgg cgtgatgaaa 1380
ctgctgcgcg acgtagcgac agcgaaaccg gcgtatgcgt tcgtcgacga agcacgacgg 1440
acgagtgccg cgaaggcggt cgaaaaagga atcgagtgcg tactgaagac gcaggtggtt 1500
gtgaatggcc ggcgaccgt gtggtgtgcg caacatgacg aagtcacgct cgcgcctgcc 1560
ccggcgagga cgtttgaatt agtttcgctg agtgggtggtg aaagcgttga gatcgtgcg 1620
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<210> 2
 <211> 638
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (28)...(308)
 <223> Pectin methyl esterase domain

<221> DOMAIN
 <222> (309)...(638)
 <223> Catalytic domain

<400> 2

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Ala Asp Gly Ser Gly Asp Val Arg Thr Ile Gln Gln Ala Val Asp Gln
 35           40           45
Val Pro Lys Asp Asn Thr His Pro Val Leu Ile Gln Ile Lys Pro Gly
 50           55           60
Val Tyr Gln Glu Gln Val Arg Val Ala Ala Gly Lys Arg Phe Ile Thr
 65           70           75           80
Phe Arg Gly Asp Asp Ala Ser Lys Thr Val Ile Thr Tyr Arg Leu Ser
 85           90           95
Ala Leu Gln Ala Gly Asn Thr Arg Leu Ala Phe Thr Thr Phe Val Asn
 100          105          110
Ala Asp Asp Phe Arg Ala Glu Asn Leu Thr Phe Glu Asn Ser Phe Gly
 115          120          125
Thr Gly Ser Gln Ala Val Ala Leu Phe Val Asp Ala Asp Arg Ala Thr
 130          135          140
Phe Glu Asn Cys Arg Phe Leu Gly Trp Gln Asp Thr Leu Phe Val Asn
 145          150          155          160
Gly Ser Arg His Phe Phe Lys Asp Cys Tyr Val Glu Gly His Val Asp
 165          170          175
Phe Ile Phe Gly Thr Ala Ser Ala Val Phe Glu Asn Cys Thr Ile His
 180          185          190
Ser Lys Gly Glu Gly Tyr Val Thr Ala His Tyr Arg Thr Ser Asp Glu

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	195		200		205
Met	Asp Thr Gly Phe Val	Phe His Arg Cys Arg	Leu Thr Gly Arg Asp		
210		215	220		
Thr	Gly Arg Gly Val Tyr	Leu Gly Arg Pro Trp	Arg Pro Tyr Ala Arg		
225		230	235		240
Val	Val Phe Ile Asp Cys Trp	Leu Asp Ala His Ile	Arg Pro Glu Gly		
	245	250	255		
Trp	Asp Asn Trp Arg Asp	Pro Glu Arg Glu Lys	Thr Ala Trp Phe Ala		
	260	265	270		
Glu	Tyr Lys Ser Lys Gly	Pro Gly Ala Asn Pro	Val Ala Arg Val Ala		
	275	280	285		
Trp	Ser Arg Gln Leu Thr	Thr Glu Gln Ala Ala	Glu Phe Ser Arg Glu		
290		295	300		
Arg	Phe Phe Ser Arg Ala	Val Arg Gly Leu Ser	Gly Gln Ala Asn Gln		
305		310	315		320
Ala	Val Gly Thr Ile Ala	Trp Asp Asp Ala	Gln Lys Lys Pro Asn	Glu	
	325	330	335		
Trp	Tyr Ala Ser Ala Glu	Ala Leu Arg Ile Ala	Asp Asn Val Val Leu		
	340	345	350		
Tyr	Gln Arg Asp Ser Gly	Gly Trp Pro Lys Asn	Ile Asp Met Gly Lys		
	355	360	365		
Pro	Leu Asp Glu Lys Gly	Arg Ala Gly Leu Leu	Arg Val Arg Lys Lys		
	370	375	380		
Asn	Asp Ser Thr Ile Asp	Asn Gly Ala Thr Tyr	Thr Gln Leu Ser Phe		
385		390	395		400
Leu	Ala Arg Val Tyr Thr	Ala Gln Lys Gln Glu	Arg His Arg Glu Ser		
	405	410	415		
Phe	Leu Lys Gly Leu Asp	Tyr Leu Leu Lys	Ala Gln Tyr Pro Asn	Gly	
	420	425	430		
Gly	Trp Pro Gln Phe Tyr	Pro Asn Leu Asn Gly	Tyr Tyr Lys His Ile		
	435	440	445		
Thr	Phe Asn Asp Asn Ala	Met Ile Gly Val Met	Lys Leu Leu Arg Asp		
	450	455	460		
Val	Ala Thr Ala Lys Pro	Ala Tyr Ala Phe Val	Asp Glu Ala Arg Arg		
465		470	475		480
Thr	Ser Ala Ala Lys Ala	Val Glu Lys Gly Ile	Glu Cys Ile Leu Lys		
	485	490	495		
Thr	Gln Val Val Val Asn	Gly Arg Arg Thr Val	Trp Cys Ala Gln His		
	500	505	510		
Asp	Glu Val Thr Leu Ala	Pro Ala Pro Ala Arg	Thr Phe Glu Leu Val		
	515	520	525		
Ser	Leu Ser Gly Gly Glu	Ser Val Glu Ile Val	Arg Phe Leu Met Ser		
	530	535	540		
Ile	Lys Asn Pro Ser Pro	Ala Val Val Glu Ala	Ile Glu Ser Ala Val		
545		550	555		560
Ala	Trp Phe Glu Gln Ser	Gln Val Lys Asp Pro	Ala Gly Lys Pro Ala		
	565	570	575		
Trp	Ala Arg Phe Tyr Glu	Ile Gly Thr Asn Arg	Pro Ile Phe Ala Gly		
	580	585	590		
Arg	Asp Gly Val Val Lys	Tyr Asp Val Lys Gln	Ile Asp Glu Glu Arg		
	595	600	605		
Arg	Lys Asn Tyr Ala Trp	Tyr Val Asp Asp Ala	Ala Lys Leu Leu Lys		
	610	615	620		
Thr	Asp Tyr Pro Glu Trp	Lys Glu Lys Asn Ala	Lys Asp Gln		
625		630	635		

<210> 3

<211> 1416

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 3

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atcgtgaaac	gcatcaagcg	acctcgtttc	ccgatgcgca	cgtttgatct	cacggagttt	180
ggagcgaaag	gtgatggacg	aacagattgc	acgttggttt	tccgtcgcgc	gatcgatcga	240
tgcacgaacg	ccggtgggtg	gagagtagtt	gttccaccgg	gttcgtatct	caactggcgc	300
attcatttga	agagcaacgt	cgaccttcat	atctcagaag	gtactacggt	caagttcagc	360
cagaacccga	aagactacct	gcccgttggt	ttctcgcgtt	gggaaggcgt	cgagggtgtt	420
aactactcgc	cttttatcta	cgccttcgaa	caaacgaaca	ttgcgatcac	tggcaagggc	480
acgctcaacg	gtcaaagcga	caacgaacac	tggtggccct	ggaacggacg	tgccgcgtac	540
ggctggaaa	aagggatgag	caatcagcgt	cccgatcgaa	atgcgctggt	tgcgatggcc	600
gaaaaaggtg	tcccggttca	ggagcgcatt	tttgggtgagg	gccattactt	aaggccgcag	660
ttcattcaac	cttatcgttg	tgagaacgtg	ctgatcgaag	gtgtcactat	tcgaaactcg	720
ccgatgtggg	aaattcatcc	ggtgctctgc	cggaatgtca	tcgtccaaaa	tgtgatcatc	780
aacagtcatg	gtccaaacaa	cgacgggtgt	aatcctgagt	cgtgcacgga	tgtgttgatt	840
aaggattgtg	acttcgacac	tggtgacgat	tgtatcgcga	tcaagtcagg	ccgaaatgca	900
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gatggtcacg	gcgggattac	ggtgggcagc	gagatttcgg	gtgggggtgcg	aaatcttttc	1020
gcatccaact	gccggctcga	cagtccgaac	ctggaccatg	cattgcgggt	taagaataac	1080
gctatgcgtg	gcgggctggt	ggagaatctg	cacttccgaa	atatcgacgt	cgggcaagtg	1140
gcgcacgcgg	tgatcacgat	cgatttcaat	tatgaggaag	gcgcgaaggg	atcgttcacg	1200
ccagtcgttc	gtgattacac	cgtcgatggc	cttcgcagca	cgaaaagtaa	gtacgcgctc	1260
gatgtgcagg	gcttggcgac	ggcgccgatc	gtgaatctgc	gtctaaccaa	ctgcatcttc	1320
gacaatgtcg	ctgaaggaaa	tgttgtagaag	aacgtaaagg	atgcaactat	cgagaatgtc	1380
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<210> 4

<211> 471

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(28)

<221> DOMAIN

<222> (81)...(476)

<223> Catalytic domain

<400> 4

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Leu	Ile	Ala	Val	Ala	Pro	Arg	Leu	Ser	Ala	Phe	Ala	Ala	Glu	Glu	Asn
		20					25						30		
Pro	Trp	Glu	Thr	Val	Met	Pro	Ser	Ile	Val	Lys	Arg	Ile	Lys	Arg	Pro
		35				40					45				
Arg	Phe	Pro	Met	Arg	Thr	Phe	Asp	Leu	Thr	Glu	Phe	Gly	Ala	Lys	Gly
	50				55					60					
Asp	Gly	Arg	Thr	Asp	Cys	Thr	Leu	Ala	Phe	Arg	Arg	Ala	Ile	Asp	Arg
65					70				75					80	
Cys	Thr	Asn	Ala	Gly	Gly	Gly	Arg	Val	Val	Pro	Pro	Gly	Ser	Tyr	
		85						90					95		

Leu	Thr	Gly	Ala	Ile	His	Leu	Lys	Ser	Asn	Val	Asp	Leu	His	Ile	Ser
			100					105					110		
Glu	Gly	Thr	Thr	Val	Lys	Phe	Ser	Gln	Asn	Pro	Lys	Asp	Tyr	Leu	Pro
			115				120					125			
Val	Val	Phe	Ser	Arg	Trp	Glu	Gly	Val	Glu	Val	Phe	Asn	Tyr	Ser	Pro
			130				135				140				
Phe	Ile	Tyr	Ala	Phe	Glu	Gln	Thr	Asn	Ile	Ala	Ile	Thr	Gly	Lys	Gly
145					150					155					160
Thr	Leu	Asn	Gly	Gln	Ser	Asp	Asn	Glu	His	Trp	Trp	Pro	Trp	Asn	Gly
				165					170					175	
Arg	Ala	Ala	Tyr	Gly	Trp	Lys	Glu	Gly	Met	Ser	Asn	Gln	Arg	Pro	Asp
			180					185					190		
Arg	Asn	Ala	Leu	Phe	Ala	Met	Ala	Glu	Lys	Gly	Val	Pro	Val	Gln	Glu
			195				200					205			
Arg	Ile	Phe	Gly	Glu	Gly	His	Tyr	Leu	Arg	Pro	Gln	Phe	Ile	Gln	Pro
			210			215					220				
Tyr	Arg	Cys	Glu	Asn	Val	Leu	Ile	Glu	Gly	Val	Thr	Ile	Arg	Asn	Ser
225				230						235					240
Pro	Met	Trp	Glu	Ile	His	Pro	Val	Leu	Cys	Arg	Asn	Val	Ile	Val	Gln
				245					250					255	
Asn	Val	Ile	Ile	Asn	Ser	His	Gly	Pro	Asn	Asn	Asp	Gly	Cys	Asn	Pro
			260				265						270		
Glu	Ser	Cys	Thr	Asp	Val	Leu	Ile	Lys	Asp	Cys	Asp	Phe	Asp	Thr	Gly
			275				280					285			
Asp	Asp	Cys	Ile	Ala	Ile	Lys	Ser	Gly	Arg	Asn	Ala	Asp	Gly	Arg	Arg
			290			295					300				
Leu	Lys	Ala	Pro	Thr	Glu	Asn	Ile	Ile	Val	Thr	Gly	Cys	Arg	Met	Lys
305					310					315					320
Asp	Gly	His	Gly	Gly	Ile	Thr	Val	Gly	Ser	Glu	Ile	Ser	Gly	Gly	Val
				325					330					335	
Arg	Asn	Leu	Phe	Ala	Ser	Asn	Cys	Arg	Leu	Asp	Ser	Pro	Asn	Leu	Asp
			340				345						350		
His	Ala	Leu	Arg	Val	Lys	Asn	Asn	Ala	Met	Arg	Gly	Gly	Leu	Leu	Glu
			355				360					365			
Asn	Leu	His	Phe	Arg	Asn	Ile	Asp	Val	Gly	Gln	Val	Ala	His	Ala	Val
			370			375					380				
Ile	Thr	Ile	Asp	Phe	Asn	Tyr	Glu	Glu	Gly	Ala	Lys	Gly	Ser	Phe	Thr
385				390						395					400
Pro	Val	Val	Arg	Asp	Tyr	Thr	Val	Asp	Gly	Leu	Arg	Ser	Thr	Lys	Ser
				405					410					415	
Lys	Tyr	Ala	Leu	Asp	Val	Gln	Gly	Leu	Ala	Thr	Ala	Pro	Ile	Val	Asn
			420				425					430			
Leu	Arg	Leu	Thr	Asn	Cys	Ile	Phe	Asp	Asn	Val	Ala	Glu	Gly	Asn	Val
			435				440					445			
Val	Lys	Asn	Val	Lys	Asp	Ala	Thr	Ile	Glu	Asn	Val	Lys	Ile	Asn	Gly
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Lys	Ser	Val	Asp	Ala	Val	Pro									
465					470										

<210> 5

<211> 1077

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

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60

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gtgatccttt atcaacgcga caacggtggt tggccgaaga atatcgacat ggccgccatg 180
ctcatgcagg cagaacgcga aaaacttagt cgcgagaaga gcgagaccga cacgacaatc 240
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atcgaaagcc atcgcgtcgc gtttttcaaa ggccctcgatt ttcttttcgc catgcagtac 360
gggaatggcg gcttcccgcga attttttcct ctgctgacg attattcgcg cgagattacg 420
ttcaacgaca acgcatgat aaatgtgctt cggttgctcc gcgacatagc cgatcgaag 480
aacgattatg tgtttgtcga tgaagagcgg cgagcgaagg ccgagcaggc tgtaaggcgt 540
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ttgaccgccc gcgagagcgt tggcatcgtc cggtttttga tgctagaaaa accaacaccc 720
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gtatccgaac cgaatgagtt gttgaatgaa gattatccga agtggaggac aaggagtgcg 1020
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<210> 6
 <211> 358
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(358)
 <223> Catalytic domain

<400> 6

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		20						25					30		
Glu	Ala	Thr	Arg	Ile	Ala	Asn	Gln	Val	Ile	Leu	Tyr	Gln	Arg	Asp	Asn
		35					40					45			
Gly	Gly	Trp	Pro	Lys	Asn	Ile	Asp	Met	Ala	Ala	Met	Leu	Met	Gln	Ala
	50				55						60				
Glu	Arg	Glu	Lys	Leu	Ser	Arg	Glu	Lys	Ser	Glu	Thr	Asp	Thr	Thr	Ile
65					70					75					80
Asp	Asn	Gly	Ala	Thr	Thr	Thr	Gln	Leu	Ala	Tyr	Leu	Ala	Lys	Val	Ile
			85						90					95	
Thr	Ala	Lys	Asn	Ile	Glu	Ser	His	Arg	Val	Ala	Phe	Phe	Lys	Gly	Leu
		100						105					110		
Asp	Phe	Leu	Phe	Ala	Met	Gln	Tyr	Gly	Asn	Gly	Gly	Phe	Pro	Gln	Phe
		115					120					125			
Phe	Pro	Leu	Arg	Asp	Asp	Tyr	Ser	Arg	Glu	Ile	Thr	Phe	Asn	Asp	Asn
	130					135					140				
Ala	Met	Ile	Asn	Val	Leu	Arg	Leu	Leu	Arg	Asp	Ile	Ala	Asp	Arg	Lys
145					150					155					160
Asn	Asp	Tyr	Val	Phe	Val	Asp	Glu	Glu	Arg	Ala	Lys	Ala	Glu	Gln	
			165						170					175	
Ala	Val	Arg	Arg	Ala	Ile	Pro	Leu	Ile	Leu	Ser	Thr	Gln	Val	Val	Val
		180						185					190		
Asp	Gly	Lys	Lys	Thr	Val	Trp	Ala	Ala	Gln	Tyr	Asp	Glu	Lys	Thr	Leu
		195					200					205			
Lys	Pro	Ala	Ala	Ala	Arg	Lys	Phe	Glu	Pro	Ala	Ser	Leu	Thr	Ala	Gly
	210					215					220				

Glu Ser Val Gly Ile Val Arg Phe Leu Met Leu Glu Lys Pro Thr Pro
 225 230 235 240
 Glu Ile Ile Asn Ala Ile Glu Ser Ala Ile Ala Trp Tyr Lys Ala Asn
 245 250 255
 Asn Ile Ser Gly Leu Arg Trp Glu Arg Asn Gly Glu Asn Ile Val
 260 265 270
 Ile Lys Asp Lys Asn Ala Pro Pro Val Trp Ala Arg Phe Tyr Gln Ile
 275 280 285
 Glu Thr Met Arg Pro Ile Phe Ala Gly Arg Asp Ala Val Ile Arg Tyr
 290 295 300
 Asp Val Met Gln Ile Glu Ser Glu Arg Arg Asn Gly Tyr Ala Trp Tyr
 305 310 315 320
 Val Ser Glu Pro Asn Glu Leu Leu Asn Glu Asp Tyr Pro Lys Trp Arg
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 Thr Arg Ser Ala Lys Arg Ala Gln Ile Phe Gln Arg Pro Pro Leu Gly
 340 345 350
 Ser Arg Phe Arg Thr Val
 355

<210> 7
 <211> 1125
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

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 gcccgcgccg ccgtgtcccg ggggatcgac gtcatactga agaccaagt gaaacagaac 660
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<210> 8
 <211> 374
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(374)
 <223> Catalytic domain

<400> 8

Met His Ala Gly Ala Lys His Val Ser Arg Trp Arg Glu Glu Phe Leu
 1 5 10 15
 Arg Asp Phe Ala Ala Arg Leu Ser Arg Thr Ile Pro Ser Ser Pro Ala
 20 25 30
 Gln Ser Ala Ala Val Ser Gly Val Pro Ala Ala Ile Arg Trp Gly Ala
 35 40 45
 Asp Val Leu Arg Gln Lys Pro Glu Trp Tyr Ala Ser Arg Glu Ala Arg
 50 55 60
 Thr Ile Ala Asp Ser Val Ile Gln Tyr Gln Ala Ala Asp Gly Gly Trp
 65 70 75 80
 Pro Lys Asn Thr Asp Leu Gly Thr Pro Pro Thr Ala Glu Ser Arg Ala
 85 90 95
 Gly Ala Ala Ala Asp Val Thr Ser Ser Thr Ile Asp Asn Asn Gly Thr
 100 105 110
 Thr Met Pro Met Gln Phe Leu Ala Leu Val Ala Asp Ala Thr Gly Glu
 115 120 125
 Ala Arg Tyr Arg Ala Ser Phe Leu Arg Gly Phe Asp Tyr Leu Leu Ala
 130 135 140
 Ala Gln Tyr Pro Asn Gly Gly Trp Pro Gln Phe Phe Pro Leu Arg Arg
 145 150 155 160
 Gly Tyr Tyr Thr His Ile Thr Phe Asn Asp Asn Ala Met Val Asn Val
 165 170 175
 Leu Thr Val Leu Arg Asp Ala Ala Ala Gly Gln Ala Pro Tyr Ala Phe
 180 185 190
 Val Asp Glu Pro Arg Arg Ala Lys Ala Arg Ala Ala Val Ser Arg Gly
 195 200 205
 Ile Asp Val Ile Leu Lys Thr Gln Val Lys Gln Asn Gly Lys Leu Thr
 210 215 220
 Ala Trp Cys Ala Gln His Asp Glu Lys Thr Leu Ala Pro Ala Trp Ala
 225 230 235 240
 Arg Ala Tyr Glu Pro Pro Ser Leu Ser Gly Ser Glu Thr Val Gly Ile
 245 250 255
 Val Arg Phe Leu Met Glu Ile Glu Lys Pro Ser Pro Glu Ile Val Ala
 260 265 270
 Ala Ile Glu Gly Ala Val Ala Trp Leu Lys Ser Val Ala Ile Pro Gly
 275 280 285
 Leu Arg Tyr Glu Ser Phe Thr Gly Ala Asp Gly Gln Arg Asp Arg Arg
 290 295 300
 Val Val Pro Asp Pro Ser Ala Gly Leu Leu Trp Ala Arg Phe Tyr Glu
 305 310 315 320
 Leu Gly Thr Asn Arg Pro Ile Phe Leu Gly Arg Asp Ser Val Val Arg
 325 330 335
 Ala Ala Leu Ser Asp Ile Glu Arg Glu Arg Arg Ala Gly Tyr Ala Tyr
 340 345 350
 Tyr Gly Thr Trp Pro Ala Ser Leu Ile Ala Ala Asp Tyr Pro Arg Trp
 355 360 365
 Arg Ser Thr Leu Arg Arg
 370

<210> 9

<211> 1116

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample


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<400> 9
ttgatcggtg gcatgaaaac gattctctca aatctgaacg cggcgctgct ttcatgcgcc      60
ctgctctttg cggcagccac acaggaacc aagccgccg aagtgcggtg gaatgagtg      120
ctaaaccaa aacctgcctg gtacggcagc ccggaagcgg tgcgcattgc tgacaacctg      180
ttgctttacc aacgcgacca cggcggtggt cacaagaata tcgaaatggc tgcggtcttg      240
accgaacagc aacaggcaga gttgaaagcg caaaaggcaa ccgacgattc gacgattgat      300
aacggcgcg cctataccca ggtgatttat ctggcgcgcg tcttcaatgc gacgaagcag      360
gagcgattca aaaccgcgtt tctcaaagga ttcgattatc tgctcaaggc tcagtatgcg      420
aacggcggtt ggccgcagta ttaccgcgtt ttgcagggtt attacaaaca catcacgttc      480
aacgatgacg cgatggtcgg cgtgcttgat cttctgcgcg atgttgcgcg cggcgattcc      540
ggttatcggg tcgtggacag cgaccggcgc gcccgcgcca gccaggccgt gcaaaaagga      600
attgagtgca tcttgaaatg ccagatcgtg gtccgcggga aaaagaccgc ctggtgcgcg      660
caacacgatg aagtgcattt cggcccgcg ccggcacgca cctacgagaa aatttcgctg      720
agcggcagcg aatcggttgg cctgatccgc ttctgatgg gcattgaaca accggacgcg      780
cgtgtagttg aggcgattga gtccgcggtt gcctggctca agcaagccaa gctgaccggc      840
atcaaagtgg ttcagaaggc ggatgcttcg aagcccaatg gcttcgaccg ggtcgtcgtt      900
gaagatgcac aagccgggcc attgtgggcg cgcttttacg agatcggtac gggccgcccg      960
atcttttccg gacgtgacgg catcgtcaaa tacagcttgg cggaaatcga acacgaacgg     1020
cgcacggggt acggctggta cacgaatgcg cccgcgaaat tgctggaaca agattatccg     1080
gcctggcaaa tcaaacgcgg gggcaagaaa aagtaa                                1116

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<210> 10
<211> 371
<212> PRT
<213> Unknown

```

```

<220>
<223> Obtained from an environmental sample

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<221> SIGNAL
<222> (1)...(29)

```

```

<221> DOMAIN
<222> (30)...(371)
<223> Catalytic domain

```

```

<400> 10
Met Ile Gly Ser Met Lys Thr Ile Leu Ser Asn Leu Asn Ala Ala Leu
 1           5           10           15
Leu Ser Cys Ala Leu Leu Phe Ala Ala Ala Thr Gln Gly Thr Lys Pro
          20          25          30
Pro Glu Val Arg Trp Asn Glu Cys Leu Asn Gln Lys Pro Ala Trp Tyr
          35          40          45
Gly Ser Pro Glu Ala Val Arg Ile Ala Asp Asn Leu Leu Leu Tyr Gln
          50          55          60
Arg Asp His Gly Gly Trp His Lys Asn Ile Glu Met Ala Ala Val Leu
65          70          75          80
Thr Glu Gln Gln Gln Ala Glu Leu Lys Ala Gln Lys Ala Thr Asp Asp
          85          90          95
Ser Thr Ile Asp Asn Gly Ala Thr Tyr Thr Gln Val Ile Tyr Leu Ala
          100          105          110
Arg Val Phe Asn Ala Thr Lys Gln Glu Arg Phe Lys Thr Ala Phe Leu
          115          120          125
Lys Gly Phe Asp Tyr Leu Leu Lys Ala Gln Tyr Ala Asn Gly Gly Trp
          130          135          140
Pro Gln Tyr Tyr Pro Arg Leu Gln Gly Tyr Tyr Lys His Ile Thr Phe
145          150          155          160
Asn Asp Asp Ala Met Val Gly Val Leu Asp Leu Leu Arg Asp Val Ala
          165          170          175

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Arg Gly Asp Ser Gly Tyr Arg Phe Val Asp Ser Asp Arg Arg Ala Arg
 180 185 190
 Ala Ser Gln Ala Val Gln Lys Gly Ile Glu Cys Ile Leu Lys Cys Gln
 195 200 205
 Ile Val Val Ala Gly Lys Lys Thr Ala Trp Cys Ala Gln His Asp Glu
 210 215 220
 Val Thr Phe Ala Pro Ala Pro Ala Arg Thr Tyr Glu Lys Ile Ser Leu
 225 230 235 240
 Ser Gly Ser Glu Ser Val Gly Leu Ile Arg Phe Leu Met Gly Ile Glu
 245 250 255
 Gln Pro Asp Ala Arg Val Val Glu Ala Ile Glu Ser Ala Val Ala Trp
 260 265 270
 Leu Lys Gln Ala Lys Leu Thr Gly Ile Lys Val Val Gln Lys Ala Asp
 275 280 285
 Ala Ser Lys Pro Asn Gly Phe Asp Arg Val Val Val Glu Asp Ala Gln
 290 295 300
 Ala Gly Pro Leu Trp Ala Arg Phe Tyr Glu Ile Gly Thr Gly Arg Pro
 305 310 315 320
 Ile Phe Ser Gly Arg Asp Gly Ile Val Lys Tyr Ser Leu Ala Glu Ile
 325 330 335
 Glu His Glu Arg Arg Thr Gly Tyr Gly Trp Tyr Thr Asn Ala Pro Ala
 340 345 350
 Lys Leu Leu Glu Gln Asp Tyr Pro Ala Trp Gln Ile Lys Arg Gly Gly
 355 360 365
 Lys Lys Lys
 370

<210> 11
 <211> 1167
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 11
 atgtcggttg gaccaggtgc taatccgaaa gctcgcggttc cctgggtccaa acaactatcg 60
 ggtggttgagg caaagttgtt cgatcgcgag cggttcttca gcctcgctgc ggaacgaacc 120
 tctaagaaga atgaccagca agtcggcgcc atcgcggtgga aagatgcaca cggaaaggca 180
 gatgagtggt atgagagcgt tgaggcactt cgtatagccg ataacgtcgt tttctatcaa 240
 cgtgactcag gtggctggcc caagaatata gagatggcga agacgttgag cgatcgtag 300
 aaggctgcga ttctccgcga gaagaaaaag aatgactcaa caatcgacaa tggcgcgact 360
 cacactcagt tatcttttct ggcgcgcgct tatacagcac aacagcagga gcgacatcg 420
 gagtcatttt taaaaggact ggattactta ctgaaggcgc agtattcaaa tggtagctgg 480
 ccacagttct atccaaactt gaatggctac tacaacgga tcacgtacaa cgatggcgcg 540
 atgatcggtg tgatgaagct tctgcggtgat gttgcggcag cgaaacctga atacgcgttt 600
 gtcgatgaaa ctcggcgtgc gaaggctgcg aacgcggttg aaaaaggcat cgtgtgcatt 660
 ttgaaaacgc aggtggttgt tgatgggcgt cgcactgttt ggtgtgcaca acacgacgaa 720
 gtgacgtttg cgcccgcgcc tgcaagaaag tttgagttag cttcgttgag cggcggtag 780
 agcgctcgata ttgttcgatt tctaattgtc ataaaggatc catcgcgtaa cgtggttgaa 840
 tcgattgaat cggcagttaa atggtttgag cagtcggagc taaaaggcgt taagtgggtc 900
 aagaaaaccg acgctactca acctaattggg ttcgattgtg tcggttgtaa agatccggag 960
 agctctgttt gggcgcgctt ttacgagatt ggcacgaacc gcccgatctt tgccgggctg 1020
 gatggagtg ctaagtatga cgtcgcgag atcgaacacg agcgacgaac gggttacgaa 1080
 tggtagcttg atgagcgagc aaaactgctg aaaaaagatt atccggcgtg gaagaaacga 1140
 catgtcgtca cgacgcgagt tcattag 1167

<210> 12
 <211> 388

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (1)...(388)

<223> Catalytic domain

<400> 12

Met	Ser	Leu	Gly	Pro	Gly	Ala	Asn	Pro	Lys	Ala	Arg	Val	Pro	Trp	Ser
1				5					10					15	
Lys	Gln	Leu	Ser	Gly	Val	Glu	Ala	Lys	Leu	Phe	Asp	Arg	Glu	Arg	Phe
		20						25					30		
Phe	Ser	Leu	Ala	Ala	Glu	Arg	Thr	Ser	Lys	Lys	Asn	Asp	Gln	Gln	Val
		35					40					45			
Gly	Ala	Ile	Ala	Trp	Lys	Asp	Ala	His	Gly	Lys	Ala	Asp	Glu	Trp	Tyr
		50				55					60				
Ala	Ser	Val	Glu	Ala	Leu	Arg	Ile	Ala	Asp	Asn	Val	Val	Phe	Tyr	Gln
65					70					75					80
Arg	Asp	Ser	Gly	Gly	Trp	Pro	Lys	Asn	Ile	Glu	Met	Ala	Lys	Thr	Leu
				85					90					95	
Ser	Asp	Arg	Glu	Lys	Ala	Ala	Ile	Leu	Arg	Glu	Lys	Lys	Lys	Asn	Asp
			100					105					110		
Ser	Thr	Ile	Asp	Asn	Gly	Ala	Thr	His	Thr	Gln	Leu	Ser	Phe	Leu	Ala
		115					120					125			
Arg	Val	Tyr	Thr	Ala	Gln	Gln	Glu	Arg	His	Arg	Glu	Ser	Phe	Leu	
		130				135				140					
Lys	Gly	Leu	Asp	Tyr	Leu	Leu	Lys	Ala	Gln	Tyr	Ser	Asn	Gly	Gly	Trp
145					150					155					160
Pro	Gln	Phe	Tyr	Pro	Asn	Leu	Asn	Gly	Tyr	Tyr	Lys	Arg	Ile	Thr	Tyr
				165				170						175	
Asn	Asp	Gly	Ala	Met	Ile	Gly	Val	Met	Lys	Leu	Leu	Arg	Asp	Val	Ala
			180					185					190		
Ala	Ala	Lys	Pro	Glu	Tyr	Ala	Phe	Val	Asp	Glu	Thr	Arg	Arg	Ala	Lys
		195					200					205			
Ala	Ala	Asn	Ala	Val	Glu	Lys	Gly	Ile	Val	Cys	Ile	Leu	Lys	Thr	Gln
		210				215					220				
Val	Val	Val	Asp	Gly	Arg	Arg	Thr	Val	Trp	Cys	Ala	Gln	His	Asp	Glu
225				230						235					240
Val	Thr	Phe	Ala	Pro	Ala	Pro	Ala	Arg	Lys	Phe	Glu	Leu	Ala	Ser	Leu
				245					250					255	
Ser	Gly	Gly	Glu	Ser	Val	Asp	Ile	Val	Arg	Phe	Leu	Met	Ser	Ile	Lys
			260					265					270		
Asp	Pro	Ser	Arg	Asn	Val	Val	Glu	Ser	Ile	Glu	Ser	Ala	Val	Lys	Trp
		275					280					285			
Phe	Glu	Gln	Ser	Glu	Leu	Lys	Gly	Val	Lys	Trp	Val	Lys	Lys	Thr	Asp
	290					295					300				
Ala	Thr	Gln	Pro	Asn	Gly	Phe	Asp	Cys	Val	Val	Val	Lys	Asp	Pro	Glu
305					310					315					320
Ser	Ser	Val	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Arg	Pro	Ile
				325					330					335	
Phe	Ala	Gly	Arg	Asp	Gly	Val	Pro	Lys	Tyr	Asp	Val	Ala	Gln	Ile	Glu
		340						345					350		
His	Glu	Arg	Arg	Thr	Gly	Tyr	Glu	Trp	Tyr	Val	Asp	Glu	Ala	Ala	Lys
		355					360					365			
Leu	Leu	Lys	Lys	Asp	Tyr	Pro	Ala	Trp	Lys	Lys	Arg	His	Val	Val	Thr
	370					375					380				

Thr Arg Val His
385

<210> 13
<211> 1065
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 13
atgaaaacga tcagccttat ttgcctcgca atctctgctg ggattctgga ttcggttgcg 60
gcggcacgct ggaacgaatt cgcccagaag gcgcatgatt ggtatcgagg tgacgaaggc 120
aggcgcgttg cttcgaatat tctttctcac caatcactgc aaggaagctg gcccaagaat 180
accgatacca ccgcgagatt cttcaatgga gatctagcga agattcaggg cacgttcgac 240
aacggtgcga cgacggacga gttgcgtttc ctggcccgcg cgtttgtcgc cacgaaagaa 300
aaaaactacg agtcagcgtt ccgaaaaggc ttcgaacaca ttctcgcgcg gcaatacgcg 360
aacggcggat ggccgcaata ttccgccgcg cccaaaagtt accaccgaca cattaccttc 420
aacgataaatt cgatggtgcg gctgatgatt ttcttccgcg aggtcacgac ttcgaatctc 480
tactcggttcg tcgaagcgcc gctgcgaaca caagcccgcg aaagtttcga tcgcggtgtg 540
cgggtgcattc ttaagtgccg gatcgctcgtg aacgggcaca agaccgcgtg gtgcgcgcaa 600
catgatgaaa cggatttcag cccccgatcc gcgcgtagtt acgaactgcc ttcgctgagc 660
ggttctgaat cagtcggcat tgtgcgcttg ctgatgagcc tcgatcagcc gagccgcgga 720
gtgatcgatg ccatacacia cgcgtagcgc tggttcgaat cggcgaagct gcccgggatc 780
aaaaccgttc aagagaccga tccgaattcg cccaaaaggct ggaatcgcgt cgtcgtaaaa 840
gatgaaagtg cccgaccgat gtgggcgcgt ttctacgaca tcaacaccaa caaacggttc 900
ttttgtgatc gcgatggtgt gccaaagccg agtcttgccg agatcggtta tgaacggcgg 960
aacggttatg cgtggctcgg atactggcct gaagacttgc tcgcaagaga gtatccagcg 1020
tggaagatga agtggctgaa gcccaaagag cgcccagcat tttga 1065

<210> 14
<211> 354
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(22)

<221> DOMAIN
<222> (23)...(354)
<223> Catalytic domain

<400> 14
Met Lys Thr Ile Ser Leu Ile Cys Leu Ala Ile Ser Ala Gly Ile Leu
1 5 10 15
Asp Ser Val Ala Ala Arg Trp Asn Glu Phe Ala Gln Lys Ala Asp
20 25 30
Asp Trp Tyr Arg Gly Asp Glu Gly Arg Arg Val Ala Ser Asn Ile Leu
35 40 45
Ser His Gln Ser Leu Gln Gly Ser Trp Pro Lys Asn Thr Asp Thr Thr
50 55 60
Ala Arg Phe Phe Asn Gly Asp Leu Ala Lys Ile Gln Gly Thr Phe Asp
65 70 75 80
Asn Gly Ala Thr Thr Asp Glu Leu Arg Phe Leu Ala Arg Ala Phe Val
85 90 95

Ala Thr Lys Glu Lys Asn Tyr Glu Ser Ala Phe Arg Lys Gly Phe Glu
 100 105 110
 His Ile Leu Ala Ala Gln Tyr Ala Asn Gly Gly Trp Pro Gln Tyr Ser
 115 120 125
 Pro Pro Pro Lys Ser Tyr His Arg His Ile Thr Phe Asn Asp Asn Ser
 130 135 140
 Met Val Arg Leu Met Ile Phe Leu Arg Glu Val Thr Thr Ser Asn Leu
 145 150 155 160
 Tyr Ser Phe Val Glu Ala Pro Leu Arg Thr Gln Ala Arg Glu Ser Phe
 165 170 175
 Asp Arg Gly Val Arg Cys Ile Leu Lys Cys Gln Ile Val Val Asn Gly
 180 185 190
 His Lys Thr Ala Trp Cys Ala Gln His Asp Glu Thr Asp Phe Ser Pro
 195 200 205
 Arg Ser Ala Arg Ser Tyr Glu Leu Pro Ser Leu Ser Gly Ser Glu Ser
 210 215 220
 Val Gly Ile Val Arg Leu Leu Met Ser Leu Asp Gln Pro Ser Arg Gly
 225 230 235 240
 Val Ile Asp Ala Ile Thr Asn Ala Val Ala Trp Phe Glu Ser Ala Lys
 245 250 255
 Leu Pro Gly Ile Lys Thr Val Gln Glu Thr Asp Pro Asn Ser Pro Lys
 260 265 270
 Gly Trp Asn Arg Val Val Val Lys Asp Glu Ser Ala Arg Pro Met Trp
 275 280 285
 Ala Arg Phe Tyr Asp Ile Asn Thr Asn Lys Pro Phe Phe Cys Asp Arg
 290 295 300
 Asp Gly Val Pro Lys Pro Ser Leu Ala Glu Ile Gly Tyr Glu Arg Arg
 305 310 315 320
 Asn Gly Tyr Ala Trp Leu Gly Tyr Trp Pro Glu Asp Leu Leu Ala Arg
 325 330 335
 Glu Tyr Pro Ala Trp Lys Met Lys Trp Leu Lys Pro Lys Glu Arg Pro
 340 345 350
 Ala Phe

<210> 15
 <211> 1575
 <212> DNA
 <213> Bacteria

<400> 15
 atgagacgac cagtcgcact ccggtccac gcggcactgg ccaccctggc cctggcgggc 60
 gcgaccggcg tgggtgctctc gatccccag gcatcgggcg cgcccgggcg cgccaccggc 120
 tacgccggcc agaacggcg caccaccggc ggtgccggcg gccagaccgt acggggccacc 180
 acggggcaccg ccatccacgc ggccctgtgc ggacgggcca gcagcagcac cccgatcacg 240
 atcgaggtcg agggaacgat caaccacgcc aacaccgcca aggtgtccgg cccagctgc 300
 aacaccgccc ccggagtgat cgagctgaag cagatcagca acgtcacgct cgtcggggtc 360
 ggctccggcg ccgtcttcga ccaactcggc atccacatcc gcgagtcag caacatcatc 420
 atccagaacg tgacggtccg gaacgtcaag aagtcgggct cgccgctgtc caacggcggc 480
 gacgccatcg gcatggagag cgacgtccgc aacgtctggg tcgaccactc caccctggag 540
 gcctcgggcg gcgagtcga gggctacgac ggcctcttcg acatgaagga caacaccgg 600
 tacgtgaccc tgtcgtacag catcctgcgc aaatccgggc gcggcggcct cgtgggggtcc 660
 agcgagaccg aactctcgaa cagcttcac acgtaccacc acaacctgta cgagaacatc 720
 gactcgcgcg cggccctgct gcgcggcggg accgcccaca tgtacaacaa ccactacctg 780
 cggatcaacg agtccggcat caactcccgt gccggagccc acgccaaggt ggacaacaac 840
 tacttcgagg actccaagga cgtcctcggc acctcttaca ccgacgccgc cgggtactgg 900
 caggtcagcg gcaacgtcta cgacaacgtg acctgggtccg cccggggcac cgacaacaac 960
 ccggcgggggc cggaccgcga gtccaacacc accgtctcca tcccctacgc cttcagcctc 1020
 gaccgggcca cctgcgtgcc ggacgtcgtg agccgaacgg cgggtgccgg caagggactt 1080

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cagggtgtcga acggcagctg ctccccgcag acacccacgc ccacgccgac gggcacgccg 1140
accacacccg cgccgacgac tcccaccccg agcccgacgc cctccacgcc cggaccgacc 1200
cagcccggcg ggacgaacct cagcatcggt gccgggtccg acggttcgag caaggccgac 1260
ggcaccagct acggcaacgt ccgggacggg gacctcggca cccactggtc tccggccggt 1320
tcgaccggct ccgtgtcgat caagtggggc agcgccacca cggctctccc catcgtcatc 1380
cgcgaggcgg cgggcgcgac gggcgtcatc ggctcctggc tcgtcctgaa cggcgacacc 1440
ggcgccgtgc tgacctccg cagcggggcg gggacgatct ccgtcccccg gacggccctg 1500
aagaagatca ccttcgagat cacgggcgcg agcggcacgc cacggatcgc cgagttcgag 1560
acgtacgccg gctag 1575

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<210> 16
<211> 524
<212> PRT
<213> Bacteria

```

```
<220>
```

```

<221> SIGNAL
<222> (1)...(33)

```

```

<221> DOMAIN
<222> (34)...(359)
<223> Catalytic domain

```

```
<400> 16
```

```

Met Arg Arg Pro Val Ala Leu Arg Leu His Ala Ala Leu Ala Thr Leu
 1          5          10          15
Ala Leu Ala Ala Thr Gly Val Val Leu Ser Ile Pro Gln Ala Ser
 20          25          30
Ala Ala Ala Gly Gly Ala Thr Gly Tyr Ala Gly Gln Asn Gly Gly Thr
 35          40          45
Thr Gly Gly Ala Gly Gly Gln Thr Val Arg Ala Thr Thr Gly Thr Ala
 50          55          60
Ile His Ala Ala Leu Cys Gly Arg Ala Ser Ser Thr Pro Ile Thr
 65          70          75          80
Ile Glu Val Glu Gly Thr Ile Asn His Ala Asn Thr Ala Lys Val Ser
 85          90          95
Gly Pro Ser Cys Asn Thr Ala Ala Gly Val Ile Glu Leu Lys Gln Ile
100          105          110
Ser Asn Val Thr Leu Val Gly Val Gly Ser Gly Ala Val Phe Asp Gln
115          120          125
Leu Gly Ile His Ile Arg Glu Ser Ser Asn Ile Ile Ile Gln Asn Val
130          135          140
Thr Val Arg Asn Val Lys Lys Ser Gly Ser Pro Leu Ser Asn Gly Gly
145          150          155          160
Asp Ala Ile Gly Met Glu Ser Asp Val Arg Asn Val Trp Val Asp His
165          170          175
Ser Thr Leu Glu Ala Ser Gly Gly Glu Ser Glu Gly Tyr Asp Gly Leu
180          185          190
Phe Asp Met Lys Asp Asn Thr Arg Tyr Val Thr Leu Ser Tyr Ser Ile
195          200          205
Leu Arg Lys Ser Gly Arg Gly Gly Leu Val Gly Ser Ser Glu Thr Glu
210          215          220
Leu Ser Asn Ser Phe Ile Thr Tyr His His Asn Leu Tyr Glu Asn Ile
225          230          235          240
Asp Ser Arg Ala Pro Leu Leu Arg Gly Gly Thr Ala His Met Tyr Asn
245          250          255
Asn His Tyr Leu Arg Ile Asn Glu Ser Gly Ile Asn Ser Arg Ala Gly
260          265          270

```

Ala His Ala Lys Val Asp Asn Asn Tyr Phe Glu Asp Ser Lys Asp Val
 275 280 285
 Leu Gly Thr Phe Tyr Thr Asp Ala Ala Gly Tyr Trp Gln Val Ser Gly
 290 295 300
 Asn Val Tyr Asp Asn Val Thr Trp Ser Ala Arg Gly Thr Asp Asn Asn
 305 310 315 320
 Pro Ala Gly Pro Asp Pro Gln Ser Asn Thr Thr Val Ser Ile Pro Tyr
 325 330 335
 Ala Phe Ser Leu Asp Pro Ala Thr Cys Val Pro Asp Val Val Ser Arg
 340 345 350
 Thr Ala Gly Ala Gly Lys Gly Leu Gln Val Ser Asn Gly Ser Cys Ser
 355 360 365
 Pro Gln Thr Pro Thr Pro Thr Thr Gly Thr Pro Thr Thr Pro Ala
 370 375 380
 Pro Thr Thr Pro Thr Pro Ser Pro Thr Pro Ser Thr Pro Gly Pro Thr
 385 390 395 400
 Gln Pro Gly Gly Thr Asn Leu Ser Ile Gly Ala Gly Ser Asp Gly Ser
 405 410 415
 Ser Lys Ala Asp Gly Thr Ser Tyr Gly Asn Val Arg Asp Gly Asp Leu
 420 425 430
 Gly Thr His Trp Ser Pro Ala Gly Ser Thr Gly Ser Val Ser Ile Lys
 435 440 445
 Trp Gly Ser Ala Thr Thr Val Ser Arg Ile Val Ile Arg Glu Ala Ala
 450 455 460
 Gly Ala Thr Gly Val Ile Gly Ser Trp Leu Val Leu Asn Gly Asp Thr
 465 470 475 480
 Gly Ala Val Leu Thr Ser Gly Ser Gly Ala Gly Thr Ile Ser Val Pro
 485 490 495
 Arg Thr Ala Leu Lys Lys Ile Thr Phe Glu Ile Thr Gly Ala Ser Gly
 500 505 510
 Thr Pro Arg Ile Ala Glu Phe Glu Thr Tyr Ala Gly
 515 520

<210> 17

<211> 1047

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 17

ttgccgcgtg	cgcccgggtg	tgagtcgtca	tcgccagcgc	agacgtcatc	ggttgcggtc	60
tcctgggata	agatcctccg	tcagcctgcg	gcctgggtacg	gcggtgcgga	ggcgttgcca	120
gtcgtgaga	acgtgtcttt	gtatcagcgc	gcggcaggag	ggtggccgaa	gaacatcaac	180
atggcggcgc	cgatgaccgc	cgctgaccgt	gcgaaagtca	cggacgagcg	cgcgacagac	240
gacgccacga	tcgacaacac	gtcaacgacg	acgcagatcc	gttttcttgc	gtcgtgtctt	300
cgcggcaccg	ccgacgcacg	attcaaggac	gcggcgctga	agggcatcga	cttcctgctg	360
gctgcgcaat	acgcgaatgg	aggctggcct	cagtattttc	ccctgcgcga	cgactactcg	420
cggcgcatca	cgttcaatga	cgacgcgatg	gtgaatgtga	tgacgtgct	gcgcgagact	480
tcgcagggcc	agacgcggtt	cgagttcgtc	gacgcctcgc	ggcgcgcccg	ggcggcgcag	540
tctgtctcac	gcggcgctga	cgatcatgctg	cgcacgcaga	ttcgagtcaa	cgcggtgctg	600
accggctggg	gccagcagca	cgacgagcgg	aactttcagc	cggtgaaggc	gcgcgcgtac	660
gaacatccgt	cgattgccag	caaggaaacc	gcgagcatcg	caagattcct	gatggggatt	720
gaacggccgt	cgccggagat	cgtgtccgcg	gtggatggcg	cagtcgcgtg	ggtgcgagcg	780
gcgcagattt	caggtgtgcg	gacggagcgc	cggcccgcgc	gatcgaatcc	ggcggcgcag	840
gtcgtggcgg	tgcaggactc	cgccgcgcgc	ccaatctggg	cccgtttcta	cgagattggc	900
accaaccggc	cgatgttttc	gggtcgcgac	ggcgctcatca	agtacagcct	cagcgagatc	960
gagatcgagc	ggcgcgctgg	atacagctgg	tacggcgact	acgccgccag	actgctcaga	1020

gacgactatc cgaagtggaa gaaatga

1047

<210> 18
 <211> 348
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(348)
 <223> Catalytic domain

<400> 18
 Met Pro Arg Ala Pro Gly Gly Glu Ser Ser Ser Pro Ala Gln Thr Ser
 1 5 10 15
 Ser Val Ala Val Ser Trp Asp Gln Ile Leu Arg Gln Pro Ala Ala Trp
 20 25 30
 Tyr Gly Gly Ala Glu Ala Leu Arg Val Ala Glu Asn Val Leu Leu Tyr
 35 40 45
 Gln Arg Ala Ala Gly Gly Trp Pro Lys Asn Ile Asn Met Ala Ala Pro
 50 55 60
 Met Thr Ala Ala Asp Arg Ala Lys Val Thr Asp Glu Arg Ala Gln Asn
 65 70 75 80
 Asp Ala Thr Ile Asp Asn Thr Ser Thr Thr Thr Gln Ile Arg Phe Leu
 85 90 95
 Ala Leu Val Leu Arg Gly Thr Ala Asp Ala Arg Phe Lys Asp Ala Ala
 100 105 110
 Leu Lys Gly Ile Asp Phe Leu Leu Ala Ala Gln Tyr Ala Asn Gly Gly
 115 120 125
 Trp Pro Gln Tyr Phe Pro Leu Arg Asp Asp Tyr Ser Arg Arg Ile Thr
 130 135 140
 Phe Asn Asp Asp Ala Met Val Asn Val Met Thr Leu Leu Arg Glu Thr
 145 150 155 160
 Ser Gln Gly Gln Thr Pro Phe Glu Phe Val Asp Ala Ser Arg Arg Gly
 165 170 175
 Arg Ala Ala Gln Ser Val Ser Arg Gly Val Asp Val Met Leu Arg Thr
 180 185 190
 Gln Ile Arg Val Asn Gly Val Leu Thr Gly Trp Cys Gln Gln His Asp
 195 200 205
 Glu Arg Asn Phe Gln Pro Val Lys Ala Arg Ala Tyr Glu His Pro Ser
 210 215 220
 Ile Ala Ser Lys Glu Thr Ala Ser Ile Ala Arg Phe Leu Met Gly Ile
 225 230 235 240
 Glu Arg Pro Ser Pro Glu Ile Val Ser Ala Val Asp Gly Ala Val Ala
 245 250 255
 Trp Leu Arg Ala Ala Gln Ile Ser Gly Val Arg Thr Glu Arg Arg Pro
 260 265 270
 Asp Gly Ser Asn Pro Gly Gly Asp Val Val Ala Val Gln Asp Ser Ala
 275 280 285
 Ala Pro Pro Ile Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg Pro
 290 295 300
 Met Phe Ser Gly Arg Asp Gly Val Ile Lys Tyr Ser Leu Ser Glu Ile
 305 310 315 320
 Glu Ile Glu Arg Arg Ala Gly Tyr Ser Trp Tyr Gly Asp Tyr Ala Ala
 325 330 335
 Arg Leu Leu Arg Asp Asp Tyr Pro Lys Trp Lys Lys
 340 345

<210> 19
 <211> 1122
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 19
 gtgaacaggt ggcgcgaaga cttcttgccg gacttcgcgg cccgcatgct ccggtgcatg 60
 gttccccggc cgcagatcca ctggggcggc ggtgtcatcc ggcaggaacc ggaatggtac 120
 ggctcggccg aggcgcgtgc gatcgccgac agcgttcttc aataccagtc gaccgctggc 180
 ggctggccca agaacaccga cttgacggtc tcgccaccgt ccgccgaatt ccttgccgat 240
 gcggatggtc tcacgaacac gatcgacaac gacgccacca cgttgccgat gcgatttctc 300
 gctctggtgg cgcacgcgac cggcggcatc aagtaccgcg ccgcgttcga acgcggtctg 360
 gactacctgc tcgccgctca gtatcccaat ggcggctggc ctcagtattt tcccctgcgt 420
 gacggctatt actcgacat cactacaac gacaatgcga tggtaacgt cctcaccgtt 480
 ctgcgcgatg cggccgcggg ccggccccct tactcgttcg tcgacagggc ccggcgcgcc 540
 agagcagaaa cggccatcgc tcgcggcatc gacatcatcg tgcgactca ggtgagacgg 600
 gccggcgtgc tgaccgatg gtgcgcccag cacgacgaaa agacgctcga gccggcgtgg 660
 gcgcgcaact acgaaccgcc gacactctcc gggcacgaaa gcgtcggcat cgtgcgcttt 720
 ctcatgggaa tcgaaaagcc cacgccgagg atcgtcgcgg cggtgcaagg cgccgctgac 780
 tggttgagag ccgtcgcgat cagcgggttg cgtctcgagg aattcaccga cgccgatggc 840
 aggcgcgaca ggcgcgtcgt cgccgatccg gcagcgcgc tcctgtgggc gcgcttctac 900
 gagcttgga cggaccgtcc cgtcttcacc ggccgcgaca aggtgatccg gtactcgctc 960
 agcgaaatcg agcacgagcg ccggaacggg tatgcctact atggcacatg gccggccacg 1020
 ctccctcagc aggagtaccc ccgttggcgc gcgaaacacc tggctcgacg gagcgtcagg 1080
 caggtagagg agggaatcgc gatacgcgtc cctaaccct ga 1122

<210> 20
 <211> 373
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(373)
 <223> Catalytic domain

<400> 20
 Met Asn Arg Trp Arg Glu Asp Phe Leu Arg Asp Phe Ala Ala Arg Met
 1 5 10 15
 Leu Arg Cys Met Val Pro Arg Pro Gln Ile His Trp Gly Gly Gly Val
 20 25 30
 Ile Arg Gln Glu Pro Glu Trp Tyr Gly Ser Ala Glu Ala Arg Ala Ile
 35 40 45
 Ala Asp Ser Val Leu Gln Tyr Gln Ser Thr Ala Gly Gly Trp Pro Lys
 50 55 60
 Asn Thr Asp Leu Thr Val Ser Pro Pro Ser Ala Glu Phe Leu Ala Asp
 65 70 75 80
 Ala Asp Gly Leu Thr Asn Thr Ile Asp Asn Asp Ala Thr Thr Leu Pro
 85 90 95
 Met Arg Phe Leu Ala Leu Val Ala His Ala Thr Gly Gly Ile Lys Tyr
 100 105 110
 Arg Ala Ala Phe Glu Arg Gly Leu Asp Tyr Leu Leu Ala Ala Gln Tyr
 115 120 125

Pro Asn Gly Gly Trp Pro Gln Tyr Phe Pro Leu Arg Asp Gly Tyr Tyr
 130 135 140
 Ser His Ile Thr Tyr Asn Asp Asn Ala Met Val Asn Val Leu Thr Val
 145 150 155 160
 Leu Arg Asp Ala Ala Gly Arg Pro Pro Tyr Ser Phe Val Asp Arg
 165 170 175
 Ala Arg Arg Ala Arg Ala Glu Thr Ala Ile Ala Arg Gly Ile Asp Ile
 180 185 190
 Ile Val Arg Thr Gln Val Arg Arg Ala Gly Val Leu Thr Ala Trp Cys
 195 200 205
 Ala Gln His Asp Glu Lys Thr Leu Glu Pro Ala Trp Ala Arg Asn Tyr
 210 215 220
 Glu Pro Pro Thr Leu Ser Gly His Glu Ser Val Gly Ile Val Arg Phe
 225 230 235 240
 Leu Met Gly Ile Glu Lys Pro Thr Pro Arg Ile Val Ala Ala Val Gln
 245 250 255
 Gly Ala Ala Asp Trp Leu Arg Ala Val Ala Ile Ser Gly Leu Arg Leu
 260 265 270
 Glu Glu Phe Thr Asp Ala Asp Gly Arg Arg Asp Arg Val Val Ala
 275 280 285
 Asp Pro Ala Ala Pro Leu Leu Trp Ala Arg Phe Tyr Glu Leu Gly Thr
 290 295 300
 Asp Arg Pro Val Phe Thr Gly Arg Asp Lys Val Ile Arg Tyr Ser Leu
 305 310 315 320
 Ser Glu Ile Glu His Glu Arg Arg Asn Gly Tyr Ala Tyr Tyr Gly Thr
 325 330 335
 Trp Pro Ala Thr Leu Leu Ser Glu Glu Tyr Pro Arg Trp Arg Ala Lys
 340 345 350
 His Leu Ala Arg Arg Ser Val Arg Gln Val Glu Glu Gly Ile Ala Ile
 355 360 365
 Arg Val Pro Asn Pro
 370

<210> 21

<211> 1269

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 21

atgcgtaaat	cgaactgggc	cgtcacaacg	gccatcctgc	tcgcgctgag	cgccgcaccg	60
ctggcgggcaa	agcccatcgg	acagatcacc	ctcgcgctgc	cgctcagccc	ggcgcgctg	120
accgaaacgc	cgcttgagca	gcgggcgcaa	tggcaggcct	atctcgccac	caccgaggca	180
cagcttaagg	cagacaaggc	ggcgctggct	gccgagcgcg	ccggtctggc	cgaaatcccc	240
gccaagccga	agaccggcag	cgccaacacc	atgccgctcg	acaagccgct	ggaatggtac	300
gcgtcggtccg	aggcgcgctc	ggtcgccgat	aatatcgtea	gctatcagac	tccggcaggc	360
ggctggggga	aaaatcaggc	ccgcaacgaa	cccacgcggg	tgaaaggtea	ggcctacact	420
atcgatgacg	ccgatcccac	cggttcgggc	aaatggaact	tcgtcggcac	catcgacaac	480
gacgccacca	tcgtggaaat	tcgctttctc	gcccgcgtag	cggcgggcgg	cacggggccc	540
gaaggcgacg	tctatcgcg	ctccgccacg	cgccgcatca	cctacttgct	ggcgggcgag	600
taccccaatg	gcggctggcc	gcaggctctg	ccgcttcagg	gcggctatca	cgacgccatc	660
accctcaatg	acggcgcgat	gatccatgtg	ctcgaactgt	ttgacgacat	cgccagcgga	720
cagggcgact	tcgccttcct	gcctgagccg	ctgcgcgaca	aggtcgaggc	cgcacaggca	780
aagggtcaga	aggtgcttct	cgatcttcag	cttaagcgca	acggcgaacg	caccctgtgg	840
gcgcagcagt	acgatccgat	taccctcttg	cccagcgcg	cgcgtaacta	cgagccgtcg	900
tcgatcagca	ccggtgaaag	cgccggtgtg	ctgatctacc	tcatgtccct	gccaacccc	960
tcgcctgaag	tgcgcgacgc	catcgaaaaa	ggcgtggccc	tgctgatcaa	acttcagatc	1020

```

aacggcatgg catgggaaaa ggacggcatg cgcaaacgtc tggtcgccaa ggctgacgcc 1080
tcgccgctgt ggtcgcgcta tcacgactcg gaaacgctgc tgcccatctt cggtgaccgc 1140
gacatgcgca tcttcgacga cgtcaacgac atcagcgacg aacgcagccg cggctatgcc 1200
tggtatggca caagcccggc acggggccatc gccgaatacg aaaaatggaa acagggcaac 1260
ggcaaatga 1269

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```

<210> 22
<211> 422
<212> PRT
<213> Unknown

```

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<220>
<223> Obtained from an environmental sample

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```

<221> SIGNAL
<222> (1)...(23)

<221> DOMAIN
<222> (24)...(422)
<223> Catalytic domain

```

```

<400> 22
Met Arg Lys Ser Asn Trp Ala Val Thr Thr Ala Ile Leu Leu Ala Leu
 1          5          10          15
Ser Ala Ala Pro Leu Ala Ala Lys Pro Ile Gly Gln Ile Thr Leu Ala
 20          25          30
Val Pro Leu Ser Pro Ala Arg Leu Thr Glu Thr Pro Pro Glu Gln Arg
 35          40          45
Ala Gln Trp Gln Ala Tyr Leu Ala Thr Thr Glu Ala Gln Leu Lys Ala
 50          55          60
Asp Lys Ala Ala Leu Ala Ala Glu Arg Ala Gly Leu Ala Glu Ile Pro
 65          70          75          80
Ala Lys Pro Lys Thr Gly Ser Ala Asn Thr Met Pro Leu Asp Lys Pro
 85          90          95
Leu Glu Trp Tyr Ala Ser Ser Glu Ala Arg Leu Val Ala Asp Asn Ile
100          105          110
Val Ser Tyr Gln Thr Pro Ala Gly Gly Trp Gly Lys Asn Gln Ala Arg
115          120          125
Asn Glu Pro Thr Arg Leu Lys Gly Gln Ala Tyr Thr Ile Asp Asp Ala
130          135          140
Asp Pro Thr Gly Ser Gly Lys Trp Asn Phe Val Gly Thr Ile Asp Asn
145          150          155          160
Asp Ala Thr Ile Val Glu Ile Arg Phe Leu Ala Arg Val Ala Ala Ala
165          170          175
Ala Thr Gly Pro Glu Gly Asp Val Tyr Arg Ala Ser Ala Thr Arg Gly
180          185          190
Ile Thr Tyr Leu Leu Ala Ala Gln Tyr Pro Asn Gly Gly Trp Pro Gln
195          200          205
Val Trp Pro Leu Gln Gly Gly Tyr His Asp Ala Ile Thr Leu Asn Asp
210          215          220
Gly Ala Met Ile His Val Leu Glu Leu Phe Asp Asp Ile Ala Ser Gly
225          230          235          240
Gln Gly Asp Phe Ala Phe Leu Pro Glu Pro Leu Arg Asp Lys Val Glu
245          250          255
Ala Ala Gln Ala Lys Gly Gln Lys Val Leu Leu Asp Leu Gln Leu Lys
260          265          270
Arg Asn Gly Glu Arg Thr Leu Trp Ala Gln Gln Tyr Asp Pro Ile Thr
275          280          285
Leu Leu Pro Ser Ala Ala Arg Asn Tyr Glu Pro Ser Ser Ile Ser Thr

```

290		295		300
Gly Glu Ser Ala Gly Val Leu Ile Tyr Leu Met Ser Leu Pro Asn Pro				
305		310		315
Ser Pro Glu Val Arg Asp Ala Ile Glu Lys Gly Val Ala Leu Leu Ile				
	325		330	
Lys Leu Gln Ile Asn Gly Met Ala Trp Glu Lys Asp Gly Met Arg Lys				
	340		345	
Arg Leu Val Ala Lys Ala Asp Ala Ser Pro Leu Trp Ser Arg Tyr His				
	355		360	
Asp Ser Glu Thr Leu Leu Pro Ile Phe Gly Asp Arg Asp Met Arg Ile				
	370		375	
Phe Asp Asp Val Asn Asp Ile Ser Asp Glu Arg Ser Arg Gly Tyr Ala				
385		390		395
Trp Tyr Gly Thr Ser Pro Ala Arg Ala Ile Ala Glu Tyr Glu Lys Trp				
	405		410	
Lys Gln Gly Asn Gly Lys				
	420			

<210> 23
 <211> 1182
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 23

atgaaccgtg	gcgtgattgt	tttgcctggcg	gccgctccag	ctgcggcgca	tggcgagctg	60
ctgggggtata	tgacgcctgc	gcagccgttg	accgaggcgc	gcattgccgc	gctgccggcg	120
tcggagcagg	gcgcctggcg	gggctacctc	gcccgcctcc	gcgcagccat	ggacgccgac	180
aaggccgccc	tggccgcccga	gcgcgcgcgc	ctcgccaccg	taccgccggc	gccgccgcat	240
ggcggtggtg	atggcgggat	ggcgcgcaac	cgcccgacgg	cttggtatgg	gacgccggaa	300
gcgcggcaca	tcgcggacaa	tatcgtcagc	ttccagacgc	cgccggcgcg	ctgggggcaag	360
aacgtggacc	gcacggggacc	tgtgcgccag	cgcgacagc	attacgtttc	cttcgatggc	420
aaggagtcct	ggaacttcat	cggcacgac	gacaacaacg	ccacaacgag	cgagctgaaa	480
ttcctggcgc	gcgtgcaggc	gcaaattgcc	ggcgcgcgcg	gcgacgaata	ccggaaggcc	540
gccctgcgcg	gcatcagcta	cctgttgaac	tcacaatatc	ccaacggcgc	cttcccgcag	600
gtctatccgc	tgcaaggcgg	ctaccacgac	gccatcacct	tcaacgacga	tgcttccgcc	660
aacgtgctgc	aagtgtgtgt	ggaagtggcg	aaccgcaggg	gcgactatgc	cttcgtcccc	720
gaaaccgtgg	caaccgatgc	ccgcgcggcc	gcggacaagg	cgctccaagt	cctgctggcg	780
agccagatca	tcgtcgggcg	cgtacgcacc	gcctggtgcc	agcagcacga	tgcgatcacg	840
ctggcgcccc	tcggcgcccc	caatttcgaa	ccggccgcgc	tgaccagcac	ggaaagcgcg	900
cgctgtgtga	tgctgttgat	gctgctgccc	gatccgagcc	cggagctgag	agcgtcaatc	960
catgcgggga	tggcctggct	gcagaaagcg	gcgctgccgg	gggatgtctg	gtcgcgctac	1020
tatgacctga	acacgatgag	gccgatcttt	ggggatcgct	accgcagtat	ccacgatgat	1080
gtgaaggaat	tgagcgagga	gaggcaaaaa	ggctatggct	ggttcagtaa	cggaccagcc	1140
agagctaaac	aggcttttga	ggcctggacg	cgaaacctt	ga		1182

<210> 24
 <211> 393
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(18)

<221> DOMAIN

<222> (19)...(393)

<223> Catalytic domain

<400> 24

```

Met Asn Arg Gly Val Ile Val Leu Leu Ala Ala Ala Pro Ala Ala Ala
 1          5          10          15
His Gly Ala Val Leu Gly Tyr Met Thr Pro Ala Gln Pro Leu Thr Glu
          20          25          30
Ala Arg Ile Ala Ala Leu Pro Ala Ser Glu Gln Gly Ala Trp Arg Gly
          35          40          45
Tyr Leu Ala Arg Ser Arg Ala Ala Met Asp Ala Asp Lys Ala Ala Leu
 50          55          60
Ala Ala Glu Arg Ala Ala Leu Ala Thr Val Pro Ala Pro Pro His
 65          70          75          80
Gly Gly Gly Asp Gly Gly Met Ala Arg Asn Arg Pro Thr Ala Trp Tyr
          85          90          95
Gly Thr Pro Glu Ala Arg His Ile Ala Asp Asn Ile Val Ser Phe Gln
          100          105          110
Thr Pro Ser Gly Gly Trp Gly Lys Asn Val Asp Arg Thr Gly Pro Val
          115          120          125
Arg Gln Arg Gly Gln His Tyr Val Ser Phe Asp Gly Lys Glu Ser Trp
 130          135          140
Asn Phe Ile Gly Thr Ile Asp Asn Asn Ala Thr Thr Ser Glu Leu Lys
 145          150          155          160
Phe Leu Ala Arg Val Gln Ala Gln Met Pro Gly Ala Ala Gly Asp Glu
          165          170          175
Tyr Arg Lys Ala Ala Leu Arg Gly Ile Ser Tyr Leu Leu Asn Ser Gln
          180          185          190
Tyr Pro Asn Gly Gly Phe Pro Gln Val Tyr Pro Leu Gln Gly Gly Tyr
          195          200          205
His Asp Ala Ile Thr Phe Asn Asp Asp Ala Phe Ala Asn Val Leu Gln
          210          215          220
Val Leu Leu Glu Val Ala Asn Arg Arg Gly Asp Tyr Ala Phe Val Pro
 225          230          235          240
Glu Thr Val Ala Thr Asp Ala Arg Ala Ala Ala Asp Lys Ala Leu Gln
          245          250          255
Val Leu Leu Ala Ser Gln Ile Ile Val Gly Gly Val Arg Thr Ala Trp
          260          265          270
Cys Gln Gln His Asp Ala Ile Thr Leu Ala Pro Val Gly Ala Arg Asn
          275          280          285
Phe Glu Pro Ala Ala Leu Thr Ser Thr Glu Ser Ala Arg Leu Leu Met
 290          295          300
Leu Leu Met Leu Leu Pro Asp Pro Ser Pro Glu Leu Arg Ala Ser Ile
 305          310          315          320
His Ala Gly Met Ala Trp Leu Gln Lys Ala Ala Leu Pro Gly Asp Val
          325          330          335
Trp Ser Arg Tyr Tyr Asp Leu Asn Thr Met Arg Pro Ile Phe Gly Asp
          340          345          350
Arg Asp Arg Ser Ile His Asp Asp Val Lys Glu Leu Ser Glu Glu Arg
          355          360          365
Gln Lys Gly Tyr Gly Trp Phe Ser Asn Gly Pro Ala Arg Ala Lys Gln
          370          375          380
Ala Phe Glu Ala Trp Thr Arg Lys Pro
 385          390

```

<210> 25

<211> 1194

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 25

```

ttggtcgcgtg ccctattaag ctgcggcagc gccaatctct atgcagaatc aaccgcaaaa      60
tcggttacgc aatcagcagc cacaaatcaa ttgcaaatg aaaaaagcag ttgggacagc      120
tattacgccg catccaaaaa aatacatcag gcagaccagg attttctcgc cgctgaatta      180
aaaaaactcg gtcagaaaaa accaacattg cccgcacaca ccaaagattt tgggtttgat      240
gttaagcagg taaatgcaga ttggtttaaa agtgacgaag gcaaacgtgt gatggagatt      300
attctctcct tcctaaacccc gtccggcggg ttgtcaaagc gtaccgacat ggccaaggcg      360
gtgcgacaac ctgggcaagc ctttggcgtt gaaaaaggct atatcccaac atttgataat      420
ggcgctacca gcactcaatt gatgttgctc gcgcaagcac accaagccac cggcgatcac      480
cgcttttagcg acgcattttg gcgcggcgtt caattaattt tgactgcgca ataccggaat      540
ggtggctggc cacaaaactt tccactaacc ggtagctacc acgattacat cacctacaac      600
gacaatctta cgcgcgacct gatggtagtg ctgcacaaaa cagcgcaggc aaaaaatgat      660
tttgcatctg tgaccaaaagc gcagcaaadc gcagcgtcag ctagcctcgc gcgtgcactt      720
gattgcgtat tgaaatcaca agttgtcgtc aatggcacac gcacactctg gggcgcacag      780
cacgatgtta aaacactgca accaaccaaa gcgcgcgcac ttgaaatggt gtcactcact      840
accactgaaa gcgcagccat gctcagtttt ctgatggata tcaaaaatcc cagcgcggat      900
attattcaat ccatacatgc agccatagcc tggatatgagc aaaataaaat cgtcggaaaa      960
acctggacac gtggtgatgc ggaattaaaa gataataaaa attcgcagcc actctgggcg      1020
cgtttttatg agataggcac taataagcct atatttgggg atcgcgatga cactgtgtat      1080
tacgatttgg caaaagtgtc taaagagcgt cgcgaagggt atgcgtggta ctccactgac      1140
ccgaataaga cgctaaaaaa atatgctgaa tgggtctaaaa aatatcccaa ataa      1194

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<210> 26

<211> 397

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(15)

<221> DOMAIN

<222> (16)...(397)

<223> Catalytic domain

<400> 26

```

Met Val Ala Ala Leu Leu Ser Cys Gly Ser Ala Asn Leu Tyr Ala Glu
 1           5           10           15
Ser Thr Ala Lys Ser Val Thr Gln Ser Ala Ala Thr Asn Gln Leu Gln
          20          25          30
Asn Glu Lys Ser Ser Trp Asp Ser Tyr Tyr Ala Ala Ser Lys Lys Ile
      35          40          45
His Gln Ala Asp Gln Asp Phe Leu Ala Ala Glu Leu Lys Lys Leu Gly
      50          55          60
Gln Lys Lys Pro Thr Leu Pro Ala His Thr Lys Asp Phe Gly Phe Asp
      65          70          75          80
Val Lys Gln Val Asn Ala Asp Trp Phe Lys Ser Asp Glu Gly Lys Arg
          85          90          95
Val Met Glu Ile Ile Leu Ser Phe Gln Thr Pro Ser Gly Gly Trp Ser
      100          105          110
Lys Arg Thr Asp Met Ala Lys Ala Val Arg Gln Pro Gly Gln Ala Phe
      115          120          125

```

Gly	Val	Glu	Lys	Gly	Tyr	Ile	Pro	Thr	Phe	Asp	Asn	Gly	Ala	Thr	Ser		
130						135					140						
Thr	Gln	Leu	Met	Leu	Leu	Ala	Gln	Ala	His	Gln	Ala	Thr	Gly	Asp	His		
145					150					155					160		
Arg	Phe	Ser	Asp	Ala	Phe	Gly	Arg	Gly	Leu	Gln	Leu	Ile	Leu	Thr	Ala		
				165					170						175		
Gln	Tyr	Pro	Asn	Gly	Gly	Trp	Pro	Gln	Asn	Phe	Pro	Leu	Thr	Gly	Ser		
			180					185						190			
Tyr	His	Asp	Tyr	Ile	Thr	Tyr	Asn	Asp	Asn	Leu	Thr	Arg	Asp	Leu	Met		
		195					200					205					
Val	Val	Leu	His	Lys	Thr	Ala	Gln	Ala	Lys	Asn	Asp	Phe	Ala	Phe	Val		
210						215					220						
Thr	Lys	Ala	Gln	Gln	Ile	Ala	Ala	Ser	Ala	Ser	Leu	Ala	Arg	Ala	Leu		
225					230					235					240		
Asp	Cys	Val	Leu	Lys	Ser	Gln	Val	Val	Val	Asn	Gly	Thr	Arg	Thr	Leu		
				245					250						255		
Trp	Gly	Ala	Gln	His	Asp	Val	Lys	Thr	Leu	Gln	Pro	Thr	Lys	Ala	Arg		
			260					265						270			
Ala	Phe	Glu	Met	Val	Ser	Leu	Thr	Thr	Thr	Glu	Ser	Ala	Ala	Met	Leu		
		275					280					285					
Ser	Phe	Leu	Met	Asp	Ile	Lys	Asn	Pro	Ser	Ala	Asp	Ile	Ile	Gln	Ser		
290						295					300						
Ile	His	Ala	Ala	Ile	Ala	Trp	Tyr	Glu	Gln	Asn	Lys	Ile	Val	Gly	Lys		
305					310					315					320		
Thr	Trp	Thr	Arg	Gly	Asp	Ala	Glu	Leu	Lys	Asp	Asn	Lys	Asn	Ser	Gln		
				325					330						335		
Pro	Leu	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Lys	Pro	Ile	Phe		
			340					345					350				
Gly	Asp	Arg	Asp	Asp	Thr	Val	Tyr	Tyr	Asp	Leu	Ala	Lys	Val	Ser	Lys		
		355					360					365					
Glu	Arg	Arg	Glu	Gly	Tyr	Ala	Trp	Tyr	Ser	Thr	Asp	Pro	Asn	Lys	Thr		
	370					375					380						
Leu	Lys	Lys	Tyr	Ala	Glu	Trp	Ser	Lys	Lys	Tyr	Pro	Lys					
385					390					395							

<210> 27
 <211> 1917
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 27

gtgtctctct	ttagaaaact	cgcactgccg	gttctgtgcg	gtctactgct	ttctgtcgga	60
gcagaaaccc	gagcgtcgaa	gcgcattgtc	gtggccgctg	atggatcggg	tgacgtcagg	120
acgattcaac	aagcgggtga	ccagggtccc	aaagacaata	cacacccggt	cttgattcag	180
atcaagccgg	gtgtgtatca	ggaacaagt	cgtgtcgccg	ccggcaaacg	ctttatcact	240
cttcgcggcg	acgacgcgag	caagaccgtc	atcacctatc	gattgagcgc	actacaagcg	300
ggaaataccc	ggttggcatt	caccacctta	attaatgcag	acgactttcg	cgccgagAAC	360
ctgacgtttg	aaaactcctt	cggcaccggt	tcacaagcgg	ttgctttgtt	tgtcgatgCG	420
aaccgcgcga	cgtttgaaaa	ctgccggttc	ctcgggtggc	aggacacttt	gtttgtgaac	480
ggcagccgcc	acttcttcaa	agactgctac	gtcgaaggcc	atgtcgattt	cattttcggc	540
acggcctccg	cagtgtttga	gaactgcacc	attcacagca	aaggcgaagg	ttatgtgacc	600
gcgcactatc	gcaccagcga	tgagatggat	accggttttg	tctttcatcg	ttgtcgtttg	660
accggacgag	acacgggccg	cggagtttat	ctcgggaagg	cgtggcgacc	ttacgcgcgc	720
gtcgtcttta	tcgattgtcg	gctggacgca	cacatcagac	ctgaaggctg	ggataattgg	780
agagatcctg	aacgagagaa	gaccgcgtgg	tttgccgagt	acaagtcaaa	agggcccggg	840
gctaataccc	tagctcgtgt	cgcggtgtcc	aggcagttga	cgacagaaca	agccgccgag	900

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ttttcgcggg aacgcttttt cagccgcgct gttcgcgggc tctctgggca ggccaaccag 960
gcagtcggaa cgatcgcggt ggacgatgcg cagaaaaaac cgaacgagtg gtatgcgagc 1020
gccgaggcgt tgcgcacgct cgacaacggt gttctttatc aacgtgactc cggcggtggtg 1080
cccaagaaca tcgacatggg gaagccgctc gacgacaagg gtcgagccgg tcttctgcgc 1140
gtgcgtaaga agaacgattc caccatcgat aacggcgcg cttacacgca actctcgttt 1200
ctagcgcggg tttacacggc gcaaaagcag gagcggcacg gcgagtcggt tctgaaggga 1260
ctcgattacc tgttgaaggc gcagtatcca aacggagggt ggccgcagtt ctatcccaat 1320
ctcaacggct attacaaaca catcactttc aacgacaacg cgatgatcgg cgtgatgaaa 1380
ctgctgcgcg acgtagcggc agcgaaaccg gcgtatgcgt ttgtcgacga agcacgacga 1440
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gtgaatggcc ggcgaccggt gtggtgtgcg caacatgacg aagtcacgct cgcgcctgcc 1560
ccggcgagga cgtttgaatt agtttcgctg agtggtggtg aaagcgttga gatcgtgcgc 1620
tttttgatgt cgatcaagaa cccgtcgccg gcggttgctg aggcgatcga gtcggcggtt 1680
gcgtggttcg agcaatcgca agtgaaagat cccgcccgcg aacctgcgtg ggcgcgattt 1740
tatgagatcg gcactaatcg tccgatcttc gccgggcgtg acggcgctgt taagtatgat 1800
gtgaaacaga tcgatgagga acgacgaaag aattacgcat ggtacgttga cgacgcagcg 1860
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<210> 28
 <211> 638
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (28)...(308)
 <223> Pectin methyl esterase domain

<221> DOMAIN
 <222> (309)...(638)
 <223> Catalytic domain

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<400> 28
Met Ser Leu Phe Arg Lys Leu Ala Leu Pro Val Leu Cys Gly Leu Leu
  1             5             10            15
Leu Ser Val Gly Ala Glu Thr Arg Ala Ser Lys Arg Ile Val Val Ala
  20            25            30
Ala Asp Gly Ser Gly Asp Val Arg Thr Ile Gln Gln Ala Val Asp Gln
  35            40            45
Val Pro Lys Asp Asn Thr His Pro Val Leu Ile Gln Ile Lys Pro Gly
  50            55            60
Val Tyr Gln Glu Gln Val Arg Val Ala Ala Gly Lys Arg Phe Ile Thr
  65            70            75            80
Leu Arg Gly Asp Asp Ala Ser Lys Thr Val Ile Thr Tyr Arg Leu Ser
  85            90            95
Ala Leu Gln Ala Gly Asn Thr Arg Leu Ala Phe Thr Thr Leu Ile Asn
  100           105           110
Ala Asp Asp Phe Arg Ala Glu Asn Leu Thr Phe Glu Asn Ser Phe Gly
  115           120           125
Thr Gly Ser Gln Ala Val Ala Leu Phe Val Asp Ala Asn Arg Ala Thr
  130           135           140
Phe Glu Asn Cys Arg Phe Leu Gly Trp Gln Asp Thr Leu Phe Val Asn
  145           150           155           160
Gly Ser Arg His Phe Phe Lys Asp Cys Tyr Val Glu Gly His Val Asp

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				165					170					175			
Phe	Ile	Phe	Gly	Thr	Ala	Ser	Ala	Val	Phe	Glu	Asn	Cys	Thr	Ile	His		
			180					185					190				
Ser	Lys	Gly	Glu	Gly	Tyr	Val	Thr	Ala	His	Tyr	Arg	Thr	Ser	Asp	Glu		
		195					200					205					
Met	Asp	Thr	Gly	Phe	Val	Phe	His	Arg	Cys	Arg	Leu	Thr	Gly	Arg	Asp		
	210					215					220						
Thr	Gly	Arg	Gly	Val	Tyr	Leu	Gly	Arg	Pro	Trp	Arg	Pro	Tyr	Ala	Arg		
225					230					235					240		
Val	Val	Phe	Ile	Asp	Cys	Trp	Leu	Asp	Ala	His	Ile	Arg	Pro	Glu	Gly		
				245					250					255			
Trp	Asp	Asn	Trp	Arg	Asp	Pro	Glu	Arg	Glu	Lys	Thr	Ala	Trp	Phe	Ala		
		260					265						270				
Glu	Tyr	Lys	Ser	Lys	Gly	Pro	Gly	Ala	Asn	Pro	Val	Ala	Arg	Val	Ala		
		275					280				285						
Trp	Ser	Arg	Gln	Leu	Thr	Thr	Glu	Gln	Ala	Ala	Glu	Phe	Ser	Arg	Glu		
	290					295					300						
Arg	Phe	Phe	Ser	Arg	Ala	Val	Arg	Gly	Leu	Ser	Gly	Gln	Ala	Asn	Gln		
305					310					315					320		
Ala	Val	Gly	Thr	Ile	Ala	Trp	Asp	Asp	Ala	Gln	Lys	Lys	Pro	Asn	Glu		
				325					330					335			
Trp	Tyr	Ala	Ser	Ala	Glu	Ala	Leu	Arg	Ile	Ala	Asp	Asn	Val	Val	Leu		
		340					345						350				
Tyr	Gln	Arg	Asp	Ser	Gly	Gly	Trp	Pro	Lys	Asn	Ile	Asp	Met	Gly	Lys		
	355					360					365						
Pro	Leu	Asp	Asp	Lys	Gly	Arg	Ala	Gly	Leu	Leu	Arg	Val	Arg	Lys	Lys		
	370				375						380						
Asn	Asp	Ser	Thr	Ile	Asp	Asn	Gly	Ala	Thr	Tyr	Thr	Gln	Leu	Ser	Phe		
385					390					395					400		
Leu	Ala	Arg	Val	Tyr	Thr	Ala	Gln	Lys	Gln	Glu	Arg	His	Arg	Glu	Ser		
			405				410							415			
Phe	Leu	Lys	Gly	Leu	Asp	Tyr	Leu	Leu	Lys	Ala	Gln	Tyr	Pro	Asn	Gly		
		420					425					430					
Gly	Trp	Pro	Gln	Phe	Tyr	Pro	Asn	Leu	Asn	Gly	Tyr	Tyr	Lys	His	Ile		
	435					440					445						
Thr	Phe	Asn	Asp	Asn	Ala	Met	Ile	Gly	Val	Met	Lys	Leu	Leu	Arg	Asp		
	450					455					460						
Val	Ala	Ala	Ala	Lys	Pro	Ala	Tyr	Ala	Phe	Val	Asp	Glu	Ala	Arg	Arg		
465					470					475					480		
Thr	Ser	Ala	Ala	Lys	Ala	Val	Glu	Lys	Gly	Ile	Glu	Cys	Ile	Leu	Lys		
				485					490					495			
Thr	Gln	Val	Val	Val	Asn	Gly	Arg	Arg	Thr	Val	Trp	Cys	Ala	Gln	His		
		500					505						510				
Asp	Glu	Val	Thr	Leu	Ala	Pro	Ala	Pro	Ala	Arg	Thr	Phe	Glu	Leu	Val		
	515					520						525					
Ser	Leu	Ser	Gly	Gly	Glu	Ser	Val	Glu	Ile	Val	Arg	Phe	Leu	Met	Ser		
	530					535					540						
Ile	Lys	Asn	Pro	Ser	Pro	Ala	Val	Val	Glu	Ala	Ile	Glu	Ser	Ala	Val		
545					550					555					560		
Ala	Trp	Phe	Glu	Gln	Ser	Gln	Val	Lys	Asp	Pro	Ala	Gly	Lys	Pro	Ala		
				565					570					575			
Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Arg	Pro	Ile	Phe	Ala	Gly		
		580					585					590					
Arg	Asp	Gly	Val	Val	Lys	Tyr	Asp	Val	Lys	Gln	Ile	Asp	Glu	Glu	Arg		
	595					600					605						
Arg	Lys	Asn	Tyr	Ala	Trp	Tyr	Val	Asp	Asp	Ala	Ala	Lys	Leu	Leu	Lys		
	610					615				620							
Thr	Asp	Tyr	Pro	Glu	Trp	Lys	Glu	Lys	Asn	Ala	Lys	Asp	Gln				
625					630					635							

<210> 29
 <211> 1398
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 29
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 ctcccgaac tggcggttcgg acaaaacgat ccctggaaaa ctcaataccc gcagatcctc 120
 ggcgggatca aaccgccgaa atttccgaag cgcgatttcg tcatcacgaa gttcggcgcg 180
 aaggcgggaa ccgatatgcac gcaagcgatc gctaaagccc tcgacgcttg cgcgaaagcc 240
 ggcggcgac gcgtcgctgt acccgccggc gaatttctca ccggtgcgat ccatctcaag 300
 tcgaacacca atctctacgt ctcaaaaggc gcgactctga agttttcgac cgaccccgaa 360
 aaatatctgc cgatcgttca cacgcggtgg gaagggatgg agttgatgca tctctcgccg 420
 ttcattctacg cgtacgagca gacgaacatc gcgatcaccg gcgagggcac gctcgacggc 480
 caaggcaaatt cgttcttttg gaagtggcac ggcaaccggc gatacggcgg caaccccgaa 540
 gtgatcagtc agcaaaaagc gcgggcgcgga ctttacgaga tgatggacaa gaacgtaccc 600
 gtcgcggagc gcgtgttcgg tatcgggcac tatctccggc cgcagttcat ccagccgtac 660
 aaatgtaaaga acgtcttgat cgaaggcgtg acgatcatcg actcgccgat gtgggaagtt 720
 catccggtgc tttgcgagaa tgtcaccgtc cgcaatcttc acatctcgtc gcacgggtccg 780
 aacaacgacg gctgcgatcc cgagtcgtgc aaagacgtcc tgatcgacaa ctgcttcttc 840
 gacaccgggtg acgactgcat cgcgatcaag tcgggtcgca ataacgacgg tcgtcgtctg 900
 aacacaccga ccgagaacat catcgtccgc aactgcacga tgaaagacgg tcacgggtgt 960
 atcacggtcg gaagcgagat ctccggcggc gtgcgaaact tgttcgacaa cgattgcaag 1020
 atggacagtg cggatctgtg gaccgcgctc cgggtaaaga acaacgcacg gcggggcggc 1080
 atgctggaga atttctattt ccgcaacatc accgtcgggc aagtcgcgcg tgctgtggtc 1140
 gagatcgatt tcaactatga agaaggcgcg aagggatcgt acacaccggt catgcgcaac 1200
 tacgtggtcg aggatctgac gtgcaccagc gggaaccggc ccgtcgatct gcaaggatta 1260
 gacaacgcgc caatttacga tgtgtcgctg cgtaacacga ccttcggcgc gatgaagaac 1320
 aagagcgctg tgaagaatgt ccgaggactg aagatcgaaa acgttaccgt cagcggcacg 1380
 cgcgtggaga gtttatga 1398

<210> 30
 <211> 465
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(27)

<221> DOMAIN
 <222> (77)...(459)
 <223> Catalytic domain

<400> 30
 Met Ile Asn Arg Arg Asp Phe Ile Lys Asp Leu Ile Ile Thr Ser Ala
 1 5 10 15
 Gly Val Ala Val Leu Pro Gln Leu Ala Phe Gly Gln Asn Asp Pro Trp
 20 25 30
 Lys Thr Gln Tyr Pro Gln Ile Leu Ala Arg Ile Lys Pro Pro Lys Phe
 35 40 45
 Pro Lys Arg Asp Phe Val Ile Thr Lys Phe Gly Ala Lys Ala Gly Thr
 50 55 60

Asp Ser Thr Gln Ala Ile Ala Lys Ala Leu Asp Ala Cys Ala Lys Ala
 65 70 75 80
 Gly Gly Gly Arg Val Val Val Pro Ala Gly Glu Phe Leu Thr Gly Ala
 85 90 95
 Ile His Leu Lys Ser Asn Thr Asn Leu Tyr Val Ser Lys Gly Ala Thr
 100 105 110
 Leu Lys Phe Ser Thr Asp Pro Glu Lys Tyr Leu Pro Ile Val His Thr
 115 120 125
 Arg Trp Glu Gly Met Glu Leu Met His Leu Ser Pro Phe Ile Tyr Ala
 130 135 140
 Tyr Glu Gln Thr Asn Ile Ala Ile Thr Gly Glu Gly Thr Leu Asp Gly
 145 150 155 160
 Gln Gly Lys Ser Phe Phe Trp Lys Trp His Gly Asn Pro Arg Tyr Gly
 165 170 175
 Gly Asn Pro Glu Val Ile Ser Gln Gln Lys Ala Arg Ala Arg Leu Tyr
 180 185 190
 Glu Met Met Asp Lys Asn Val Pro Val Ala Glu Arg Val Phe Gly Ile
 195 200 205
 Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro Tyr Lys Cys Lys Asn
 210 215 220
 Val Leu Ile Glu Gly Val Thr Ile Ile Asp Ser Pro Met Trp Glu Val
 225 230 235 240
 His Pro Val Leu Cys Glu Asn Val Thr Val Arg Asn Leu His Ile Ser
 245 250 255
 Ser His Gly Pro Asn Asn Asp Gly Cys Asp Pro Glu Ser Cys Lys Asp
 260 265 270
 Val Leu Ile Asp Asn Cys Phe Phe Asp Thr Gly Asp Asp Cys Ile Ala
 275 280 285
 Ile Lys Ser Gly Arg Asn Asn Asp Gly Arg Arg Leu Asn Thr Pro Thr
 290 295 300
 Glu Asn Ile Ile Val Arg Asn Cys Thr Met Lys Asp Gly His Gly Gly
 305 310 315 320
 Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val Arg Asn Leu Phe Ala
 325 330 335
 His Asp Cys Lys Met Asp Ser Ala Asp Leu Trp Thr Ala Leu Arg Val
 340 345 350
 Lys Asn Asn Ala Ser Arg Gly Gly Met Leu Glu Asn Phe Tyr Phe Arg
 355 360 365
 Asn Ile Thr Val Gly Gln Val Ala Arg Ala Val Val Glu Ile Asp Phe
 370 375 380
 Asn Tyr Glu Glu Gly Ala Lys Gly Ser Tyr Thr Pro Val Met Arg Asn
 385 390 395 400
 Tyr Val Val Glu Asp Leu Thr Cys Thr Ser Gly Asn Arg Pro Val Asp
 405 410 415
 Leu Gln Gly Leu Asp Asn Ala Pro Ile Tyr Asp Val Ser Leu Arg Asn
 420 425 430
 Thr Thr Phe Gly Ala Met Lys Asn Lys Ser Val Val Lys Asn Val Arg
 435 440 445
 Gly Leu Lys Ile Glu Asn Val Thr Val Ser Gly Thr Arg Val Glu Ser
 450 455 460
 Leu
 465

<210> 31
 <211> 1401
 <212> DNA
 <213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 31

atgatcaatc	tttatggcgt	ctttgacatc	cggacctttg	gggcccacc	ggacggagaa	60
acgccttcca	ctgcggcgat	tacggcggcc	atcgaaactt	gtgccgcggc	cgggggagga	120
gtggtctaca	tcccggccgg	acggttcctc	accggtcccc	tccgcctcaa	aagccacgtc	180
cggctccatc	tcgaggccgg	agcgcaactg	ctcttttagtc	aggaccgggc	cgattatcct	240
gttctggaga	cgaggtggga	ggggaaggag	gtcttgacct	atgcacacca	gatctacggc	300
gaggacctcg	aaggggtcgc	gattaccggt	cgggggacca	tcgacggccg	gggcgagact	360
tggtggcgac	tcttcgcgc	caaagccttc	acccatcccc	gacccgcct	catcgccctt	420
acccgctgca	aggacatcct	gatagaagga	gtaaccctcg	tcaattcacc	ggcctggacc	480
atcaatcctg	tgatgtgcga	gcgggtgacc	atcgataagg	tgactatcat	caacccgccc	540
gactcgcccc	acaccgacgg	gacgcacccc	gattcctccc	ggaacgtcta	tatcactaac	600
tgctacattg	acgtaggcga	tgactgcatc	gccatcaaag	cgggccgaga	ggactccctt	660
tatcggacgc	cttgtgaaaa	cattgtcatc	gccaactgcc	tcattgcgcca	cggtcacggc	720
ggggtggtca	tcggcagcga	gaccagcggg	ggtattcgca	aggtagtcat	taccaactgc	780
atcttcgagg	acaccgaccg	gggcattaga	cttaagtccc	ggcgcggacg	cggcgggttc	840
gtcgaggacc	tccgggcgac	gaatattatc	atggaaaagg	tgctctgtcc	cttcgtcctc	900
aacatgtact	atgataccgg	gggaggcggtg	atcgacgagc	gcgcgcatga	cttagaacct	960
catccggtaa	gcgaggctac	accctccttc	cgccgcctct	ccttcagtca	cattactgcc	1020
cgggaagtgc	aggccgccgc	ggccttcctc	tacggcctgc	ccgaacagcc	tctggaggac	1080
gtcttatttg	acgatattcg	gatagagctg	gccgccgacg	cttctcctgc	ccgtccggcc	1140
atgatgcggg	ccgtcccgcc	catgagccaa	ggtggtgtgc	tctgctacgg	tgcgcgcgcg	1200
atctccttcc	ggcacatgca	cctccgcggg	caccgcggtc	cgcccttcca	gatcgaacgc	1260
gcggaggcgg	tgacgttgat	gggctgctcg	accgacggca	gtgaagacct	ccagcttgtc	1320
ttgggtcaag	cggaggaggt	caccatccgt	gactgcacct	ttaccgcccc	gcaggacccc	1380
gcaaaagaaa	ggcaaaatta	a				1401

<210> 32

<211> 466

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (1)...(348)

<223> Catalytic domain

<400> 32

Met	Ile	Asn	Leu	Tyr	Gly	Val	Phe	Asp	Ile	Arg	Thr	Phe	Gly	Ala	Gln
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Pro	Asp	Gly	Glu	Thr	Pro	Ser	Thr	Ala	Ala	Ile	Thr	Ala	Ala	Ile	Glu
			20					25					30		
Thr	Cys	Ala	Ala	Ala	Gly	Gly	Gly	Val	Val	Tyr	Ile	Pro	Ala	Gly	Arg
			35				40					45			
Phe	Leu	Thr	Gly	Pro	Leu	Arg	Leu	Lys	Ser	His	Val	Arg	Leu	His	Leu
	50					55					60				
Glu	Ala	Gly	Ala	His	Leu	Leu	Phe	Ser	Gln	Asp	Pro	Ala	Asp	Tyr	Pro
65					70				75					80	
Val	Leu	Glu	Thr	Arg	Trp	Glu	Gly	Lys	Glu	Val	Leu	Thr	Tyr	Ala	His
				85				90						95	
Gln	Ile	Tyr	Gly	Glu	Asp	Leu	Glu	Gly	Val	Ala	Ile	Thr	Gly	Arg	Gly
			100					105					110		
Thr	Ile	Asp	Gly	Arg	Gly	Glu	Thr	Trp	Trp	Arg	Leu	Phe	Arg	Ala	Lys
		115					120					125			
Ala	Phe	Thr	His	Pro	Arg	Pro	Arg	Leu	Ile	Ala	Phe	Thr	Arg	Cys	Lys
	130					135						140			

Asp Ile Leu Ile Glu Gly Val Thr Leu Val Asn Ser Pro Ala Trp Thr
 145 150 155 160
 Ile Asn Pro Val Met Cys Glu Arg Val Thr Ile Asp Lys Val Thr Ile
 165 170 175
 Ile Asn Pro Pro Asp Ser Pro Asn Thr Asp Gly Ile Asp Pro Asp Ser
 180 185 190
 Ser Arg Asn Val Tyr Ile Thr Asn Cys Tyr Ile Asp Val Gly Asp Asp
 195 200 205
 Cys Ile Ala Ile Lys Ala Gly Arg Glu Asp Ser Leu Tyr Arg Thr Pro
 210 215 220
 Cys Glu Asn Ile Val Ile Ala Asn Cys Leu Met Arg His Gly His Gly
 225 230 235 240
 Gly Val Val Ile Gly Ser Glu Thr Ser Gly Gly Ile Arg Lys Val Val
 245 250 255
 Ile Thr Asn Cys Ile Phe Glu Asp Thr Asp Arg Gly Ile Arg Leu Lys
 260 265 270
 Ser Arg Arg Gly Arg Gly Gly Phe Val Glu Asp Leu Arg Ala Thr Asn
 275 280 285
 Ile Ile Met Glu Lys Val Leu Cys Pro Phe Val Leu Asn Met Tyr Tyr
 290 295 300
 Asp Thr Gly Gly Gly Val Ile Asp Glu Arg Ala His Asp Leu Glu Pro
 305 310 315 320
 His Pro Val Ser Glu Ala Thr Pro Ser Phe Arg Arg Leu Ser Phe Ser
 325 330 335
 His Ile Thr Ala Arg Glu Val Gln Ala Ala Ala Ala Phe Leu Tyr Gly
 340 345 350
 Leu Pro Glu Gln Pro Leu Glu Asp Val Leu Phe Asp Asp Ile Trp Ile
 355 360 365
 Glu Leu Ala Ala Asp Ala Ser Pro Ala Arg Pro Ala Met Met Arg Ala
 370 375 380
 Val Pro Pro Met Ser Gln Gly Gly Val Leu Cys Tyr Gly Ala Arg Arg
 385 390 395 400
 Ile Ser Phe Arg His Met His Leu Arg Gly His Arg Gly Pro Ala Phe
 405 410 415
 Gln Ile Glu Arg Ala Glu Ala Val Gln Leu Met Gly Cys Ser Thr Asp
 420 425 430
 Gly Ser Glu Asp Pro Gln Leu Val Leu Gly Gln Ala Glu Glu Val Thr
 435 440 445
 Ile Arg Asp Cys Thr Phe Thr Ala Gln Gln Asp Pro Ala Lys Glu Arg
 450 455 460
 Gln Asn
 465

<210> 33
 <211> 1041
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 33
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 cggattacgg ccgacaagat caacaacaag cccgactcct ggcttaccag cgacgaaggc 120
 atcaagctga tcgacaacat catcacctgg cagaaccccg aggggtggctg ggccaagtac 180
 tacgacgcga ccaatccgca caaacaaggc gaagtctacg gcgactggga cggcgtcggc 240
 accatcgaca acggctacac ctacaccgag ctgaatctcc tggcgcacgt ctacaccctc 300
 accaagcgcc cggagatcct cgattcgttc aacaagggcc tggagtttct gctcaaagcc 360
 caatacccca gcggcggtcg gccgcaacgg tttccggtgc ccaacaacta cggcaagtgc 420

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atcacgctca acgacaacgc gatggtgaac gtgatgcagt tcctgcagaa cgctcgcaaag 480
ggcaaggaag acttcgcttt cgtcgacgag cagcgctcgcg ccaaagcgaa ggaggcgttt 540
gaccgcggga tcgactgcct tctgaagctc cagattaccg tgaacggcaa gcttaccgcc 600
tgggcccagc agtatgaccc gaagacactc gccgcggcgc cgcgccgggc gtacgagctc 660
ccgggcctca gcggctgcga aagcgcgccc gtcatgcgct tgttcatgtc tttggagaac 720
cccagtcccg aagttcagcg cgccgtccac gcggcggcgg cttggtacga ggcgtcgaag 780
atcaccggca agaagctggt gcgcgagaaac aacgacgtga cactggccga cgacccaac 840
ggcgagccgc tttgggcgcg cttctacgac atcgaaacca accgcccgtt ctattgcggt 900
cgcgacggcg tgaagaagtg gtcgctggac gagatcgagc ccgaacgccg caagggctac 960
gcttgggtcc gccctgggc gacgagcgta ctggagcagt atcgcaagtg ggcggcgaag 1020
caccaccccg tgaacagttg a 1041

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<210> 34
 <211> 346
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(18)

<221> DOMAIN
 <222> (19)...(346)
 <223> Catalytic domain

<400> 34

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Met Lys Leu Arg Cys Leu Met Leu Thr Leu Leu Leu Cys Gly Ser Ala
 1           5           10           15
Phe Ala Ala Asp Arg Ile Thr Ala Asp Lys Ile Asn Asn Lys Pro Asp
          20          25          30
Ser Trp Leu Thr Ser Asp Glu Gly Ile Lys Leu Ile Asp Asn Ile Ile
      35      40      45
Thr Trp Gln Asn Pro Glu Gly Gly Trp Ala Lys Tyr Tyr Asp Ala Thr
 50          55          60
Asn Pro His Lys Gln Gly Glu Val Tyr Gly Asp Trp Asp Gly Val Gly
65          70          75          80
Thr Ile Asp Asn Gly Tyr Thr Tyr Thr Glu Leu Asn Leu Leu Ala His
          85          90          95
Val Tyr Thr Leu Thr Lys Arg Pro Glu Ile Leu Asp Ser Phe Asn Lys
      100      105      110
Gly Leu Glu Phe Leu Leu Lys Ala Gln Tyr Pro Ser Gly Gly Trp Pro
      115      120      125
Gln Arg Phe Pro Val Pro Asn Asn Tyr Gly Lys Cys Ile Thr Leu Asn
      130      135      140
Asp Asn Ala Met Val Asn Val Met Gln Phe Leu Gln Asn Val Ala Lys
145          150          155          160
Gly Lys Glu Asp Phe Ala Phe Val Asp Glu Gln Arg Arg Ala Lys Ala
          165          170          175
Lys Glu Ala Phe Asp Arg Gly Ile Asp Cys Leu Leu Lys Leu Gln Ile
      180      185      190
Thr Val Asn Gly Lys Leu Thr Ala Trp Ala Gln Gln Tyr Asp Pro Lys
      195      200      205
Thr Leu Ala Ala Ala Pro Ala Arg Ala Tyr Glu Leu Pro Gly Leu Ser
      210      215      220
Gly Cys Glu Ser Ala Pro Val Met Arg Leu Phe Met Ser Leu Glu Asn
225          230          235          240
Pro Ser Pro Glu Val Gln Arg Ala Val His Ala Ala Ala Trp Tyr

```

				245					250					255	
Glu	Ala	Ser	Lys	Ile	Thr	Gly	Lys	Lys	Leu	Val	Arg	Glu	Asn	Asn	Asp
			260					265					270		
Val	Thr	Leu	Ala	Asp	Asp	Pro	Asn	Gly	Glu	Pro	Leu	Trp	Ala	Arg	Phe
		275					280					285			
Tyr	Asp	Ile	Glu	Thr	Asn	Arg	Pro	Phe	Tyr	Cys	Gly	Arg	Asp	Gly	Val
	290					295					300				
Lys	Lys	Trp	Ser	Leu	Asp	Glu	Ile	Glu	Pro	Glu	Arg	Arg	Lys	Gly	Tyr
305					310					315					320
Ala	Trp	Val	Arg	Pro	Trp	Ala	Thr	Ser	Val	Leu	Glu	Gln	Tyr	Arg	Lys
				325					330					335	
Trp	Ala	Ala	Lys	His	Pro	Pro	Val	Asn	Ser						
			340					345							

<210>	35
<211>	1071
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<400>	35						
atgccaaaaaa	attccgacga	cgcgtggcgg	gaaaagactc	cgcccgat tg	gagtctt gtc		60
acatggagcg	acgtattcaa	acagaagcct	ctctggtacc	aaaccgacga	ggcggctcga		120
gtcgcggacc	aactcctcat	ctatcaaaaa	gagaacggcg	ggtttgagaa	gaatgtcgac		180
atggcgttga	tgctgacgca	gaaggaaaaa	gaagagctca	ccgcaaagcg	gtcagacgtc		240
tccgaaacga	cgatcgacaa	ccggaccacg	tatcctcagg	tcgcgtatct	cggtcgagta		300
atcacccgae	gccttcttaa	accttgcgcc	ccggcgatat	ttcggaata	caaagacgcc		360
ttcatacaaa	gtcttgatta	ctctgttgcc	tccagtatc	agaacggagg	atttccgcaa		420
tctaatacgt	tgaaaaaagg	ctatttacaca	cacatcacct	tcaacgcacga	cgcgatgatk		480
ggcgtcctga	aggtgcttcg	cgacatcgca	aataagaaa	aggattacgt	gttcgtggat		540
gaagcgcgaa	gacttcgcgc	cgagcaagcg	gtcgccaaag	cgctgcctct	tattctgaag		600
cttcaggttg	tcgtcgacgg	aaagaaaacc	gtctgggctg	cgcagtatga	cgagactacg		660
ctggcgcctg	cagcggctcg	caagtttgag	cccgtgtcgt	tgaccgctgg	tgagagcgtc		720
ggcatcgctc	gatacctgat	gcaggaaaaa	ccgacgccgg	agatcaccga	tgcatcgag		780
tctgcgatcg	attggtatcg	aaagaacaag	atcgacggaa	tacgttggga	gcgcatacaa		840
ggcgagaaca	cggttgtgaa	agacaaatcg	gtcccccta	tatgggcacg	gttctatcag		900
atcgaaaaca	tgcgtccgat	cttcategga	cgtgattcgg	ttaatcaagta	tgacgtgacg		960
caggtcgaag	ccgagcgtcg	gaatggttac	gcctggtacg	tcaccgcacc	gaatgaattg		1020
qtqaacqaaq	attatttgaa	gtggaagggg	aaaagcgccg	gagccaagta	g		1071

<210>	36
<211>	356
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

```
<221> DOMAIN
<222> (1)...(356)
<223> Catalytic domain
```

<400> 36
Met Pro Lys Asn Ser Asp Asp Ala Trp Arg Glu Lys Thr Pro Pro Asp
1 5 10 15
Trp Ser Leu Val Thr Trp Ser Asp Val Phe Lys Gln Lys Pro Leu Trp
20 25 30

Tyr Gln Thr Asp Glu Ala Ala Arg Val Ala Asp Gln Leu Leu Ile Tyr
 35 40 45
 Gln Lys Glu Asn Gly Gly Phe Glu Lys Asn Val Asp Met Ala Leu Met
 50 55 60
 Leu Thr Gln Lys Glu Lys Glu Glu Leu Thr Ala Lys Arg Ser Asp Val
 65 70 75 80
 Ser Glu Thr Thr Ile Asp Asn Arg Thr Thr Tyr Pro Gln Val Ala Tyr
 85 90 95
 Leu Gly Arg Val Ile Thr Ala Ser Leu Leu Lys Pro Ser Pro Pro Ala
 100 105 110
 Asn Leu Pro Lys Tyr Lys Asp Ala Phe Asn Lys Gly Leu Asp Tyr Leu
 115 120 125
 Leu Ala Ser Gln Tyr Glu Asn Gly Gly Phe Pro Gln Phe Tyr Pro Leu
 130 135 140
 Lys Lys Gly Tyr Tyr Thr His Ile Thr Phe Asn Asp Asp Ala Met Ile
 145 150 155 160
 Gly Val Leu Lys Val Leu Arg Asp Ile Ala Asn Lys Lys Glu Asp Tyr
 165 170 175
 Val Phe Val Asp Glu Ala Arg Arg Leu Arg Ala Glu Gln Ala Val Ala
 180 185 190
 Lys Ala Leu Pro Leu Ile Leu Lys Leu Gln Val Val Val Asp Gly Lys
 195 200 205
 Lys Thr Val Trp Ala Ala Gln Tyr Asp Glu Thr Thr Leu Ala Pro Ala
 210 215 220
 Ala Ala Arg Lys Phe Glu Pro Val Ser Leu Thr Ala Gly Glu Ser Val
 225 230 235 240
 Gly Ile Val Arg Tyr Leu Met Gln Glu Lys Pro Thr Pro Glu Ile Thr
 245 250 255
 Asp Ala Ile Glu Ser Ala Ile Asp Trp Tyr Arg Lys Asn Lys Ile Asp
 260 265 270
 Gly Ile Arg Trp Glu Arg Ile Lys Gly Glu Asn Thr Val Val Lys Asp
 275 280 285
 Lys Ser Ala Pro Pro Ile Trp Ala Arg Phe Tyr Gln Ile Glu Thr Met
 290 295 300
 Arg Pro Ile Phe Ile Gly Arg Asp Ser Val Ile Lys Tyr Asp Val Thr
 305 310 315 320
 Gln Val Glu Ala Glu Arg Arg Asn Gly Tyr Ala Trp Tyr Val Thr Ala
 325 330 335
 Pro Asn Glu Leu Val Asn Glu Asp Tyr Leu Lys Trp Lys Gly Lys Ser
 340 345 350
 Ala Gly Ala Lys
 355

<210> 37

<211> 1860

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 37

atgttcacta	ctactggctc	tcattgcgcc	cggaattccg	cgcgtttttc	ccttactgcg	60
atagcagccg	ctgttgcggt	gatggcaggc	acttcagcat	ttgcagctgc	gacgggtggc	120
ttctctacca	ctgatgggtg	caacgtatcg	ggcgcccgtt	cgtttactgc	atcgacttac	180
cagcaaatca	acaccattat	tgccaacgca	aaactggatg	atgcaggtaa	aaaagtcact	240
gggggtgctt	accgccttat	cattacctac	accggtaatg	aagactcgct	gattaaccag	300
atgatcaaag	accacacggt	gaattcatcg	ggcaactgcc	ctaaccgcgc	ttggagcgaa	360
gcctatcgct	acgtggaaat	ttaaagagttt	accaagggta	ttaccattca	aggcgcgaa	420


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ggttcttcag caaacttcgg cattgtgatt aataaatctg acaatgtgat tgtgcgtaat 480
atgaaaatcg gtgcgcttgc tgggtgcgagt aacgatgcgg atatgattcg tatcgacacc 540
ggcggttaacg tgtggattga tcacaacgaa ttgtttgcgg taaataatga atgtaaaggt 600
tcacccgatg gtgacctgac atttgaaagt gcgattgata ttaaaaaagc atcgcaaaat 660
attacggtgt cctacaacat tatccgcgat agtaaaaaag tagggctcga tggttcgagt 720
agcagtgata ttgcaggtgg ccgtaagatt acgttccatc acaatattta tcgcaatgtt 780
gggtgcacgtt taccgttgca acgcggtggg tggacacaca tgtataacaa tctttacgac 840
ggagttacca gctcgggtat taacgttcgt caaggtggct acgcgctaac cgagaacaac 900
tgggtccaaa atgctgtcaa cccggttacc tgccgttttg acagtagtaa ctgcggttac 960
tgggatctgc gcaacaacaa cgtgcgcaac cctgggtgatt tctccacctt caacattacc 1020
tggaccagcg gtggcaccat cgacgccacc aactggacta ccaactcaacc tttcccgatt 1080
agcattcctt acagctactc gcctgttagc ccgcagtggt tcaaagacaa gttggcaaat 1140
tatgctggtg tcggtaaaaa caatgcgcaa ttaacggcgt ctgctgcag cggaataact 1200
tcatcggtag caccttcacg agtgccagca tcatcgcgcg caccttcaag ccgttcaccc 1260
agcagtgca gcccatccag cacaccaact acatcaagct cgagttcagt tgcgcgaacc 1320
ggttcaattt cgctcggtgc aacggcaacc aacaacagca ttgtgttgag ttggtcacc 1380
aacaatgtga cgctcggttc gcaagaagtg tatcgcgata ccgacgctga tccatcgggg 1440
cgtgtgcgta tcgcatccct ggctgcttca gcgcgtatgt ataccgatag cacagcggca 1500
tcgggccaaa cctattacta ctggattaaa aataccactt ctggtgttgt caccaattcc 1560
aatgctgcat cagcgcgtat tggtagcacg gcgtccagtt ctgttgcatc aagcagctca 1620
agttcaagcg gcggcgcgcc cgtattaggt ggtactgggt attatccaag cggcttctcc 1680
aagtgcgctg atttgggcgg gacttggtca gtgtcatcgg gcgatggctg ggttgcgttt 1740
ggtcgcaaa gcaagtgggt taccaagaaa gtatcggtag gtagttcaat cgcctgtacc 1800
gttgcgcat ttggttcgga tccacagggc aaccctaaca agtgttctta caaacgttaa 1860

```

<210> 38
 <211> 619
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(35)

<221> DOMAIN
 <222> (36)...(387)
 <223> Catalytic domain

```

<400> 38
Met Phe Thr Thr Thr Gly Ser His Cys Ala Arg Asn Ser Ala Arg Phe
1      5      10      15
Ser Leu Thr Ala Ile Ala Ala Ala Val Ala Leu Met Ala Gly Thr Ser
20      25      30
Ala Phe Ala Ala Ala Thr Gly Gly Phe Ser Thr Thr Asp Gly Gly Asn
35      40      45
Val Ser Gly Ala Arg Ser Phe Thr Ala Ser Thr Tyr Gln Gln Ile Asn
50      55      60
Thr Ile Ile Ala Asn Ala Lys Leu Asp Asp Ala Gly Lys Lys Val Thr
65      70      75      80
Gly Gly Ala Tyr Pro Leu Ile Ile Thr Tyr Thr Gly Asn Glu Asp Ser
85      90      95
Leu Ile Asn Gln Met Ile Lys Asp His Thr Val Asn Ser Ser Gly Asn
100     105     110
Cys Pro Asn Pro Arg Trp Ser Glu Ala Tyr Arg Tyr Val Glu Ile Lys
115     120     125
Glu Phe Thr Lys Gly Ile Thr Ile Gln Gly Ala Asn Gly Ser Ser Ala
130     135     140

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Asn	Phe	Gly	Ile	Val	Ile	Asn	Lys	Ser	Asp	Asn	Val	Ile	Val	Arg	Asn
145					150					155					160
Met	Lys	Ile	Gly	Ala	Leu	Ala	Gly	Ala	Ser	Asn	Asp	Ala	Asp	Met	Ile
				165					170					175	
Arg	Ile	Asp	Thr	Gly	Val	Asn	Val	Trp	Ile	Asp	His	Asn	Glu	Leu	Phe
			180					185					190		
Ala	Val	Asn	Asn	Glu	Cys	Lys	Gly	Ser	Pro	Asp	Gly	Asp	Leu	Thr	Phe
		195					200					205			
Glu	Ser	Ala	Ile	Asp	Ile	Lys	Lys	Ala	Ser	Gln	Asn	Ile	Thr	Val	Ser
	210					215					220				
Tyr	Asn	Ile	Ile	Arg	Asp	Ser	Lys	Lys	Val	Gly	Leu	Asp	Gly	Ser	Ser
225					230					235					240
Ser	Ser	Asp	Ile	Ala	Gly	Gly	Arg	Lys	Ile	Thr	Phe	His	His	Asn	Ile
				245					250					255	
Tyr	Arg	Asn	Val	Gly	Ala	Arg	Leu	Pro	Leu	Gln	Arg	Gly	Gly	Trp	Thr
		260					265						270		
His	Met	Tyr	Asn	Asn	Leu	Tyr	Asp	Gly	Val	Thr	Ser	Ser	Gly	Ile	Asn
	275					280						285			
Val	Arg	Gln	Gly	Gly	Tyr	Ala	Leu	Ile	Glu	Asn	Asn	Trp	Phe	Gln	Asn
	290					295					300				
Ala	Val	Asn	Pro	Val	Thr	Cys	Arg	Phe	Asp	Ser	Ser	Asn	Cys	Gly	Tyr
305					310					315					320
Trp	Asp	Leu	Arg	Asn	Asn	Asn	Val	Arg	Asn	Pro	Gly	Asp	Phe	Ser	Thr
				325					330					335	
Tyr	Asn	Ile	Thr	Trp	Thr	Ser	Gly	Gly	Thr	Ile	Asp	Ala	Thr	Asn	Trp
		340					345						350		
Thr	Thr	Thr	Gln	Pro	Phe	Pro	Ile	Ser	Ile	Pro	Tyr	Ser	Tyr	Ser	Pro
		355					360					365			
Val	Ser	Pro	Gln	Cys	Val	Lys	Asp	Lys	Leu	Ala	Asn	Tyr	Ala	Gly	Val
	370					375					380				
Gly	Lys	Asn	Asn	Ala	Gln	Leu	Thr	Ala	Ser	Ala	Cys	Ser	Gly	Asn	Thr
385					390					395					400
Ser	Ser	Val	Ala	Pro	Ser	Ser	Val	Pro	Ala	Ser	Ser	Ala	Ala	Pro	Ser
				405					410					415	
Ser	Arg	Ser	Ser	Ser	Ser	Ala	Ala	Pro	Ser	Ser	Thr	Pro	Thr	Thr	Ser
		420						425					430		
Ser	Ser	Ser	Ser	Val	Ala	Ala	Thr	Gly	Ser	Ile	Ser	Leu	Gly	Ala	Thr
		435					440					445			
Ala	Thr	Asn	Asn	Ser	Ile	Val	Leu	Ser	Trp	Ser	Pro	Asn	Asn	Val	Thr
	450					455					460				
Leu	Gly	Ser	Gln	Glu	Val	Tyr	Arg	Asp	Thr	Asp	Ala	Asp	Pro	Ser	Gly
465					470					475					480
Arg	Val	Arg	Ile	Ala	Ser	Leu	Ala	Ala	Ser	Ala	Arg	Met	Tyr	Thr	Asp
				485					490					495	
Ser	Thr	Ala	Ala	Ser	Gly	Gln	Thr	Tyr	Tyr	Tyr	Trp	Ile	Lys	Asn	Thr
			500					505					510		
Thr	Ser	Gly	Val	Val	Thr	Asn	Ser	Asn	Ala	Ala	Ser	Ala	Arg	Ile	Gly
		515					520					525			
Ser	Thr	Ala	Ser	Ser	Ser	Val	Ala	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Gly
	530					535						540			
Gly	Ala	Pro	Val	Leu	Gly	Gly	Thr	Gly	Asp	Tyr	Pro	Ser	Gly	Phe	Ser
545					550					555					560
Lys	Cys	Ala	Asp	Leu	Gly	Gly	Thr	Cys	Ser	Val	Ser	Ser	Gly	Asp	Gly
				565					570					575	
Trp	Val	Ala	Phe	Gly	Arg	Lys	Gly	Lys	Trp	Val	Thr	Lys	Lys	Val	Ser
			580					585					590		
Val	Gly	Ser	Ser	Ile	Ala	Cys	Thr	Val	Ala	Ala	Phe	Gly	Ser	Asp	Pro
		595					600					605			
Gln	Gly	Asn	Pro	Asn	Lys	Cys	Ser	Tyr	Lys	Arg					

610

615

<210> 39
 <211> 1077
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 39
 atggcgccga tcctccgacc caacctcctt tgcacttacg cgctctgcat gggcttgctc 60
 gccgtggtga gctgcgcggc ggggcccgtg tcagcgcagc agccggcgcc atggagcacg 120
 gccatcgctgg agcaggagga gagcgcgttc gcctccccgt cgatgcgcag cgtcgccgac 180
 aacgtcgtgc gccatcagtc ggccgaaggc ggctggccta agaaccacaa tctggcggcg 240
 ccgccatcgg ggccggcgcc ggagggcgtc gccaatacga tcgacaatga tgcgacgacg 300
 ctgccgatgg agtttctggc gcgtgtgatc cagcccgcg gcgtccgata caagccggcc 360
 ttcgagcgcg ggctggatta tctgcttgcg gctcagtacg cgaacggcgg ctggccgcag 420
 ttctatccgc tgcgcggggg ctattacgat cagtgacgt tcaacgacga cgccatgatc 480
 cgggtgatga ttctgctcgg cgcagtggcg cgcggcgggg cgccctatga atttgtcgac 540
 gccgggcggc gcgcgcgcgc tgcagccgcg gtcgagcggg gcctggcgct catcctgcgc 600
 acgcagatcc ggccggcgcg gcgcgtgacg gtctggtgcg cgcagtatga cagcgccacc 660
 ttgcagcccg cctgggcgcg cgcctatgag ccgccgtccc tgtccggcgc ggaaagtgtg 720
 gggatcgtgc gctatctcat gtcgatcgac catccctcgc ccgaagtcgt cgccgccgtc 780
 gacggcgctg tggcatggct gcgcgcggcc gccattgccg gcgtgcgcgt ggagaatttc 840
 acggacgccg acggccgccc tgaccgccgc gccgtggccg acgcggggcg gccgccgatc 900
 tgggcgcggg tctacgagtt cggcgccaac cggccgatct tcctggggcg tgattccggt 960
 tttcactaca cgttcggaga aatcgagcgc gagcggcgcg caggctacaa ttattacgga 1020
 tactgggcgc gtcctgtgct ggaagactat ccggcctggc gcgcgcgcgt gcgatga 1077

<210> 40
 <211> 358
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(32)

<221> DOMAIN
 <222> (33)...(358)
 <223> Catalytic domain

<400> 40
 Met Ala Pro Ile Leu Arg Pro Asn Leu Leu Cys Thr Tyr Ala Leu Cys
 1 5 10 15
 Met Gly Leu Leu Ala Val Val Ser Cys Ala Ala Gly Pro Val Ser Ala
 20 25 30
 Gln Gln Pro Ala Pro Trp Ser Thr Ala Ile Val Glu Gln Glu Glu Ser
 35 40 45
 Ala Phe Ala Ser Pro Ser Met Arg Ser Val Ala Asp Asn Val Val Arg
 50 55 60
 His Gln Ser Ala Glu Gly Gly Trp Pro Lys Asn Thr Asn Leu Ala Ala
 65 70 75 80
 Pro Pro Ser Gly Pro Ala Pro Glu Gly Val Ala Asn Thr Ile Asp Asn
 85 90 95
 Asp Ala Thr Thr Leu Pro Met Glu Phe Leu Ala Arg Val Ile His Ala

[illegible]

<210>	41
<211>	1080
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<400>	41						
atgaaaaaatt	taaaatacag	tttagtttca	tttgtactac	tcattactat	gaatgttttt		60
acgcaagaaa	aaaaagtaac	ttggaaaagc	atcacagaaa	ataacgatga	aaattgggtt		120
gtaagcggaag	aagccaaaaa	aatagccgaa	aatgttttgt	tatatcaacg	cgatattggg		180
ggttggccaa	aaaacactga	aattcaaaat	gaactttcag	aaaaagaaaa	actaacatta		240
aaagaatttaa	aatcggatcc	aaaaggatgt	accatcgaca	atgggtgcaac	gtgtcaggaa		300
ttacttttct	tatccaaaat	atataaatcc	aatccagatg	agcgatatata	aatggctttc		360
ttaaaaggtg	tgattttacct	gattacagct	caatacaaaa	atgggtggtg	gccacaatat		420
taccctttga	gagaaggata	ttacactcat	attacttaca	acgataaatgc	aatggtgaat		480
gttttaaagt	tgttgaaaga	agttaaagat	aaatctgatt	actactcaat	tcaagcaccc		540
gatgaaattt	ccaaaatggc	tgaagtatca	tttaataaag	gagtcgattg	catattaaaa		600
acacagtaca	aacaaaatgg	aatattaacc	gcttggtgtg	cacaacatga	cagggaaaca		660
ttgaaacctg	ctaaagcaag	agcttatgaa	ttgccttcgt	taagcggaaa	agaatcagcc		720
aaaatttgtgt	tgttattaat	gtcaatcgaa	aatccatcta	aagaagtaat	tactgccgta		780
aattcagcag	ttaatttggt	tgaaaaaaca	aaaatcaacg	gaattaaaat	tgaaacatt		840
tccaccggga	aaaaggatga	aaagatataga	attgtttgtg	aaagtcctga	tgctccgccg		900
ctttggggcaa	gattttatgga	attaagtgc	aacaaaccat	ttttttgtga	tcgtgacgga		960

aagaaaaaat acagcatgtc agaaattagt caagagcgta gaaccggcta tgcatggtag 1020
 accaacgaac caaaagaagt tttaaaaaaa tacgatgatt ggaagtcatc attaaactaa 1080

<210> 42
 <211> 359
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (22)...(359)
 <223> Catalytic domain

<400> 42
 Met Lys Asn Leu Lys Tyr Ser Leu Val Ser Phe Val Leu Leu Ile Thr
 1 5 10 15
 Met Asn Val Phe Thr Gln Glu Lys Lys Val Thr Trp Lys Ser Ile Thr
 20 25 30
 Glu Asn Asn Asp Glu Asn Trp Phe Val Ser Glu Glu Ala Lys Lys Ile
 35 40 45
 Ala Glu Asn Val Leu Leu Tyr Gln Arg Asp Ile Gly Gly Trp Pro Lys
 50 55 60
 Asn Thr Glu Ile Gln Asn Glu Leu Ser Glu Lys Glu Lys Leu Thr Leu
 65 70 75 80
 Lys Glu Leu Lys Ser Asp Pro Lys Gly Cys Thr Ile Asp Asn Gly Ala
 85 90 95
 Thr Cys Gln Glu Leu Leu Phe Leu Ser Lys Ile Tyr Lys Ser Asn Pro
 100 105 110
 Asp Glu Arg Tyr Lys Met Ala Phe Leu Lys Gly Val Ile Tyr Leu Ile
 115 120 125
 Thr Ala Gln Tyr Lys Asn Gly Gly Trp Pro Gln Tyr Tyr Pro Leu Arg
 130 135 140
 Glu Gly Tyr Tyr Thr His Ile Thr Tyr Asn Asp Asn Ala Met Val Asn
 145 150 155 160
 Val Leu Lys Leu Leu Lys Glu Val Lys Asp Lys Ser Asp Tyr Tyr Ser
 165 170 175
 Ile Gln Ala Pro Asp Glu Ile Ser Lys Met Ala Glu Val Ser Phe Asn
 180 185 190
 Lys Gly Val Asp Cys Ile Leu Lys Thr Gln Tyr Lys Gln Asn Gly Ile
 195 200 205
 Leu Thr Ala Trp Cys Ala Gln His Asp Arg Glu Thr Leu Lys Pro Ala
 210 215 220
 Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu Ser Gly Lys Glu Ser Ala
 225 230 235 240
 Lys Ile Val Leu Leu Leu Met Ser Ile Glu Asn Pro Ser Lys Glu Val
 245 250 255
 Ile Thr Ala Val Asn Ser Ala Val Asn Trp Phe Glu Lys Thr Lys Ile
 260 265 270
 Asn Gly Ile Lys Ile Glu Thr Ile Ser Thr Gly Lys Lys Asp Glu Lys
 275 280 285
 Asp Arg Ile Val Val Glu Ser Pro Asp Ala Pro Pro Leu Trp Ala Arg
 290 295 300
 Phe Met Glu Leu Ser Asp Asn Lys Pro Phe Phe Cys Asp Arg Asp Gly
 305 310 315 320

Lys	Lys	Lys	Tyr	Ser 325	Met	Ser	Glu	Ile	Ser 330	Gln	Glu	Arg	Arg	Thr 335	Gly
Tyr	Ala	Trp	Tyr 340	Thr	Asn	Glu	Pro	Lys 345	Glu	Val	Leu	Lys	Lys 350	Tyr	Asp
Asp	Trp	Lys 355	Ser	Ser	Leu	Asn									

<210>	43
<211>	1902
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<400>	43					
gtggatccaa	agaattggggg	cagcgggattt	accggcgaaa	tcaaagtaac	taacaacaca	60
agccaaacag	tcaatagctg	gtctgtgtca	tggcaagagg	caggagccag	tgtaactaat	120
tcctggaatg	caaccttggg	agggacgaat	ccttataccg	caaccgggtt	aggatggaac	180
tcaaccctgg	cgccccggagc	ctctgccagt	tttggttttc	aagcaaacgg	cactgcgggg	240
gccaaaagg	taaatggcag	tttgtgtggg	gcgactgcac	catctgcagc	gaccagcaaa	300
tccagtgcga	gtgttgccgag	ttcaaagatt	gcaagttcaa	ttcaatcaag	tgcaactagc	360
agttcaaaat	cgtccagttc	tgtctcacct	tcaagcacgc	caaaatccag	tagctctgct	420
ccaacggctg	catcattcac	tattcaagaa	gagcaagccg	gtttttgccg	tgtagacggt	480
attgcaacgg	aaagtaccaa	caccggattc	accggcaacg	gctacaccaa	ttccaataat	540
gtacaagggt	ctgccattgt	gtgggcggtg	aatgcaacta	ccagtgcacg	ccatacaatt	600
actttccgct	tcgctaattg	tggcactgcg	aatcgcaatg	gctcgtagt	cattaacggc	660
ggcagcaatg	gtaattacac	ggtgcaatta	ccacgcacgg	cgagctgggc	tgactggcaa	720
acagtaaatg	tggaaattga	tttggtacaa	ggcaataaca	at ttgcaact	caccgcattg	780
actgcagatg	gcctcgcaaa	tatcgacttc	atcaaaattg	aaggagcatc	aaccaaagcg	840
ggaacctgtg	caggtgcggt	cagcagtagc	agtgttgctt	cttcggtaaa	atccagtgct	900
agcgcggcaa	gcagttctgt	accaacgaac	accggcgcca	tgctaacttt	ggatggcaac	960
cctgccgcga	gctggcttaa	caaatcgctg	acaaagtggg	gcgcatcgcg	cgctgacatt	1020
gttgctcttt	atcaacagtc	caacggcgcg	tggccaaaaa	atctggatta	caattcagtg	1080
agcgctggtt	atggcggcag	tgcaagcggc	accatcgata	atgggtgcaac	tattactgaa	1140
atggtttatc	tcgctgaggt	ttacaaaacc	ggaaacaata	ccaagtaccg	cgatgcagtt	1200
cgccgtgcag	caaactttat	cgtgagttcg	caatatagca	ctggcgcggt	gccgcaattt	1260
tatccgctca	aaggtggcta	tgcagaccac	gccaccttta	atgataacgg	catggcttac	1320
gcattaaactg	tattggattt	cgctgcaaac	aagcgcgcgc	cttttgatac	ggatgtcttt	1380
aatgacacag	accgcgcaaa	at tttaaaaca	gcgtaacca	aaggtgttga	ttacatttta	1440
aaagcgcaat	ggaaaacaaa	tggaaaatta	acagcctggt	gcgcacaaca	tggcgcgact	1500
gactatcaac	ctaaaaaagc	acgcgcttat	gaattggaat	cactgagtg	tagcgagtct	1560
gttggtgtaa	ttgcattttt	aatgacgcag	ccgcagacag	cacaaatcca	aacggccggt	1620
aaagcaggcc	tcaactgggt	caatagcccg	agcacctatt	tggaaggtta	cacctacgat	1680
tcatccaaag	cgtccactaa	tcccatagtg	cagaaagcgg	gaagtagaat	gtggtatcgc	1740
ttttacgatt	taaatacca	ccgtggtttt	ttcagcgacc	gggacggcag	caaattctat	1800
gacattacca	aaatgtctga	agaacgtcgc	acgggttata	gttggggtgg	cgcttatggt	1860
gagagatca	tcgccttttg	caaaaaaqtg	qgctatttat	aa		1902

<210>	44
<211>	633
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

```
<221> BINDING
<222> (4) ... (89)
```

<223> Carbohydrate binding module

<221> BINDING

 $\langle 222 \rangle \quad (152) \dots (275)$

<223> Carbohydrate binding module

<221> DOMAIN

 $\langle 222 \rangle \quad (277) \dots (633)$

<223> Catalytic domain

<400> 44

Met 1	Asp	Pro	Lys	Asn 5	Trp	Gly	Ser	Gly	Phe 10	Thr	Gly	Glu	Ile	Lys 15	Val
Thr	Asn	Asn	Thr 20	Ser	Gln	Thr	Val	Asn 25	Ser	Trp	Ser	Val	Ser	Trp	Gln
Glu	Ala	Gly 35	Ala	Ser	Val	Thr	Asn 40	Ser	Trp	Asn	Ala	Thr 45	Leu	Gly	Gly
Thr	Asn 50	Pro	Tyr	Thr	Ala	Thr 55	Gly	Leu	Gly	Trp	Asn 60	Ser	Thr	Leu	Ala
Pro 65	Gly	Ala	Ser	Ala 70	Ser	Phe	Gly	Phe	Gln	Ala	Asn 75	Gly	Thr	Ala	Gly
Ala	Pro	Lys	Val 85	Asn	Gly	Ser	Leu	Cys	Gly 90	Ala	Thr	Ala	Ser	Ser	Ala
Ala	Thr	Ser	Lys 100	Ser	Ser	Ala	Ser	Val 105	Ala	Ser	Ser	Lys	Ile 110	Ala	Ser
Ser	Ile 115	Gln	Ser	Ser	Ala	Thr 120	Ser	Ser	Ser	Lys	Ser 125	Ser	Ser	Ser	Ala
Ala	Pro 130	Ser	Ser	Thr	Pro	Lys 135	Ser	Ser	Ser	Ser	Ala 140	Pro	Thr	Ala	Ala
Ser 145	Phe	Thr	Ile	Gln 150	Glu	Gln	Ala	Gly	Phe 155	Cys	Arg	Val	Asp	Gly	Gly
Ile	Ala	Thr	Glu 165	Ser	Thr	Asn	Thr	Gly	Phe 170	Thr	Gly	Asn	Gly 175	Tyr	Thr
Asn	Ser	Asn 180	Asn	Val	Gln	Gly	Ala 185	Ala	Ile	Val	Trp	Ala 190	Val	Asn	Ala
Thr	Thr 195	Ser	Ala	Arg	His	Thr	Ile 200	Thr	Phe	Arg	Phe 205	Ala	Asn	Gly	Gly
Thr	Ala 210	Asn	Arg	Asn	Gly	Ser 215	Leu	Val	Ile	Asn 220	Gly	Ser	Asn	Gly	Gly
Asn 225	Tyr	Thr	Val	Gln 230	Leu	Pro	Arg	Thr	Ala 235	Ser	Trp	Ala	Asp	Trp	Gln
Thr	Val	Ser	Leu 245	Glu	Ile	Asp	Leu	Val	Gln 250	Gly	Asn	Asn	Asn 255	Leu	Gln
Leu	Thr	Ala	Leu 260	Thr	Ala	Asp	Gly	Leu 265	Ala	Asn	Ile	Asp 270	Phe	Ile	Lys
Ile	Glu 275	Gly	Ala	Ser	Thr	Lys	Ala 280	Gly	Thr	Cys	Ala 285	Gly	Ala	Val	Ser
Ser	Ser 290	Ser	Val	Ala	Ser	Ser 295	Val	Lys	Ser	Ser	Ala 300	Ser	Ala	Ala	Ser
Ser 305	Ser	Val	Pro	Thr	Asn 310	Thr	Gly	Ala	Met	Leu 315	Thr	Leu	Asp	Gly	Asn
Pro	Ala	Ala	Ser 325	Trp	Leu	Asn	Lys	Ser	Arg 330	Thr	Lys	Trp	Ser	Ala	Ser
Arg	Ala	Asp	Ile 340	Val	Ala	Ser	Tyr	Gln 345	Gln	Ser	Asn 350	Gly	Gly	Trp	Pro
Lys	Asn 355	Leu	Asp	Tyr	Asn	Ser	Val 360	Ser	Ala	Gly	Asn 365	Gly	Gly	Ser	Ala
Ser	Gly 370	Thr	Ile	Asp	Asn	Gly 375	Ala	Thr	Ile	Thr	Glu 380	Met	Val	Tyr	Leu

Ala Glu Val Tyr Lys Thr Gly Asn Asn Thr Lys Tyr Arg Asp Ala Val
 385 390 395 400
 Arg Arg Ala Ala Asn Phe Ile Val Ser Ser Gln Tyr Ser Thr Gly Ala
 405 410 415
 Leu Pro Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr
 420 425 430
 Phe Asn Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala
 435 440 445
 Ala Asn Lys Arg Ala Pro Phe Asp Thr Asp Val Phe Asn Asp Thr Asp
 450 455 460
 Arg Ala Lys Phe Lys Thr Ala Val Thr Lys Gly Val Asp Tyr Ile Leu
 465 470 475 480
 Lys Ala Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln
 485 490 495
 His Gly Ala Thr Asp Tyr Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu
 500 505 510
 Glu Ser Leu Ser Gly Ser Glu Ser Val Gly Val Ile Ala Phe Leu Met
 515 520 525
 Thr Gln Pro Gln Thr Ala Gln Ile Gln Thr Ala Val Lys Ala Gly Leu
 530 535 540
 Asn Trp Phe Asn Ser Pro Ser Thr Tyr Leu Glu Gly Tyr Thr Tyr Asp
 545 550 555 560
 Ser Ser Lys Ala Ser Thr Asn Pro Ile Val Gln Lys Ala Gly Ser Arg
 565 570 575
 Met Trp Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser
 580 585 590
 Asp Arg Asp Gly Ser Lys Phe Tyr Asp Ile Thr Lys Met Ser Glu Glu
 595 600 605
 Arg Arg Thr Gly Tyr Ser Trp Gly Gly Ala Tyr Gly Glu Ser Ile Ile
 610 615 620
 Ala Phe Gly Lys Lys Val Gly Tyr Leu
 625 630

<210> 45

<211> 987

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 45

atgactagac	gcgccttcat	cgcggttata	tgtttcttcg	cggccgtctg	cgcgacgcg	60
cagtcaccg	tgcgtggaa	ggacgtgctc	gagcagtcgc	agggctggta	ttccacgacc	120
gccgcgcacg	tcgtcgccga	cacggtgctg	ctgtatcaac	gtccatccgg	tgatggccg	180
aaggacatcg	acatgacggc	gccgcggcg	gaccgcactc	ctcccgcgcg	tccagacgcg	240
accatcgaca	acggcgccac	gaccacgcag	atccgcctgc	tcgctcgtgc	ggcctcgggc	300
gcaccggcgg	ctgccgccca	cacctacacg	gcggcgggcg	ttcgcgggat	cgattacctg	360
ctcgaggcgc	agtatcccaa	cggcggctgg	ccgcagttct	ttcccctgcg	caaggactat	420
tcgcgtacg	tcacgttcaa	cgacgacgcg	atgatgaacg	tgatgttctt	gctggacgag	480
gtctcggcgg	gagatgcgcc	gttcacgttc	gtggacgaac	aacgccgcga	ccgcgcgcgc	540
gctgcgctcg	ccaagggggg	ctccgtcatc	ctgaagtcgc	aggtccggat	cgacgggacg	600
ctgaccgcct	ggtgcgcgca	acacgacgag	atcaccctgg	caccgcgtcc	ggcgcgcacc	660
ttcgagcacg	cgtcgctcag	cggcaacgag	tctgtcgcga	tcgtgcgctt	cctgatgacc	720
cgtcgcgcga	cgccagcgat	cgtcgcgcg	gtcgatgcgg	cggtcgcctg	gctcagacgc	780
gtccgcctcc	ctgacggacg	gtgggcccg	ttctacgagt	tcggtaccaa	tcgtccgatc	840
ttctcggggc	gagacagtgt	cgtgcgctac	aaactcgagg	agatcgaaca	ggaacgtcag	900
gagggctacg	cgtggtacgg	cacgtggccg	aggacgcttg	ttgagaagat	gtaccctgca	960
tggaagtgcg	ggcttccggg	caagtag				987

<210> 46
 <211> 328
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(20)

<221> DOMAIN
 <222> (21)...(328)
 <223> Catalytic domain

<400> 46
 Met Thr Arg Arg Ala Phe Ile Ala Val Ile Cys Phe Phe Ala Ala Val
 1 5 10 15
 Cys Ala His Ala Gln Ser Thr Val Arg Trp Lys Asp Val Leu Glu Gln
 20 25 30
 Ser Glu Gly Trp Tyr Ser Thr Thr Ala Ala His Val Val Ala Asp Thr
 35 40 45
 Val Leu Leu Tyr Gln Arg Pro Ser Gly Gly Trp Pro Lys Asp Ile Asp
 50 55 60
 Met Thr Ala Pro Pro Ala Asp Arg Thr Pro Pro Ala Arg Pro Asp Ala
 65 70 75 80
 Thr Ile Asp Asn Gly Ala Thr Thr Thr Gln Ile Arg Leu Leu Ala Arg
 85 90 95
 Ala Ala Ser Gly Ala Pro Ala Ala Ala His Thr Tyr Thr Ala Ala
 100 105 110
 Ala Leu Arg Gly Ile Asp Tyr Leu Leu Glu Ala Gln Tyr Pro Asn Gly
 115 120 125
 Gly Trp Pro Gln Phe Phe Pro Leu Arg Lys Asp Tyr Ser Arg Tyr Val
 130 135 140
 Thr Phe Asn Asp Asp Ala Met Met Asn Val Met Phe Leu Leu Asp Glu
 145 150 155 160
 Val Ser Ala Gly Asp Ala Pro Phe Thr Phe Val Asp Glu Gln Arg Arg
 165 170 175
 Asp Arg Ala Arg Ala Ala Val Ala Lys Gly Val Ser Val Ile Leu Lys
 180 185 190
 Ser Gln Val Arg Ile Asp Gly Thr Leu Thr Ala Trp Cys Ala Gln His
 195 200 205
 Asp Glu Ile Thr Leu Ala Pro Arg Pro Ala Arg Thr Phe Glu His Ala
 210 215 220
 Ser Leu Ser Gly Asn Glu Ser Val Ala Ile Val Arg Phe Leu Met Thr
 225 230 235 240
 Arg Pro Pro Thr Pro Ala Ile Val Ala Ala Val Asp Ala Ala Val Ala
 245 250 255
 Trp Leu Arg Arg Val Arg Leu Pro Asp Gly Arg Trp Ala Arg Phe Tyr
 260 265 270
 Glu Phe Gly Thr Asn Arg Pro Ile Phe Ser Gly Arg Asp Ser Val Val
 275 280 285
 Arg Tyr Lys Leu Glu Glu Ile Glu Gln Glu Arg Gln Glu Gly Tyr Ala
 290 295 300
 Trp Tyr Gly Thr Trp Pro Arg Thr Leu Val Glu Lys Met Tyr Pro Ala
 305 310 315 320
 Trp Lys Ser Arg Leu Pro Gly Lys
 325

<210> 47
 <211> 1077
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 47
 atgaaaaatt ttaaaaaatat tgtaggagcg ttactttatat ctgtaacggt ttgtgtgcac 60
 gggcaggtaa acaaaaaatc ctggcgggct attacacagt ctaacgacga tgcattggtt 120
 gcatctgatg gagctgcaca gattgcagat aatgtattac tctatcagcg caatgttggc 180
 ggatggccta aaaatattga aatgcaggaa ccgcttagtg aggccgacaa aaaaaagctg 240
 atagatctta agtctacggc caaagaaagt actacagata atggggctac gtgtcaggaa 300
 atggtattcc tctctaagat atataaaca aagcccgaag agaagtataa agaggctttt 360
 ttaaaaggac ttaattattt gcttgaagca cagtataaaa atgggtggatg gccacagttc 420
 taccctttta aaaaagggtta ttatacccac attacctata atgacgattc tatggtaaac 480
 attcttatga tcttaagaa tattaaggaa gatgccaaact attacagtat tacgccaaagc 540
 gataaagttt taaagcaggt atcgacagct tttgacagag gcattgactg cattctaaaa 600
 acacagtaca agcaaaaggg tgtgcttaca agctgggtgtg cccagcacga tgagggttaca 660
 ttagaacctg caaatgcaag ggcttttgag ttggcatcac taagtggtaa agaattctgct 720
 aaaataacgt tgttgctaatt gtctgtaaaa aatccgtcta aagaggttgt tgctgctgta 780
 gatgctgctg tggcgtggtt tgaaaaaaca aaaattgaag gcattaaagt agaagaagta 840
 accggagctg atggcaaaaa ggatagggtta gtagtacaaa gggctgatgc cgaaccattg 900
 tgggcgcggt ttatggaaact ggataccaac aggccatttt tttgcgacag ggacggtata 960
 aaaaaatatt cgcttgctga gataggtcat gaacgccgta acggatatgg ctggtacacc 1020
 aacgaaccaa aagaagtttt aaagaaatac accaaatgga aaaacagtct taaatag 1077

<210> 48
 <211> 358
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (22)...(358)
 <223> Catalytic domain

<400> 48
 Met Lys Asn Phe Lys Asn Ile Val Gly Ala Leu Leu Ile Ser Val Thr
 1 5 10 15
 Phe Cys Val His Gly Gln Val Asn Lys Lys Ser Trp Arg Ala Ile Thr
 20 25 30
 Gln Ser Asn Asp Asp Ala Trp Phe Ala Ser Asp Gly Ala Ala Gln Ile
 35 40 45
 Ala Asp Asn Val Leu Leu Tyr Gln Arg Asn Val Gly Gly Trp Pro Lys
 50 55 60
 Asn Ile Glu Met Gln Glu Pro Leu Ser Glu Ala Asp Lys Lys Lys Leu
 65 70 75 80
 Ile Asp Leu Lys Ser Thr Ala Lys Glu Ser Thr Thr Asp Asn Gly Ala
 85 90 95
 Thr Cys Gln Glu Met Val Phe Leu Ser Lys Ile Tyr Lys Gln Lys Pro
 100 105 110

Glu Glu Lys Tyr Lys Glu Ala Phe Leu Lys Gly Leu Asn Tyr Leu Leu
 115 120 125
 Glu Ala Gln Tyr Lys Asn Gly Gly Trp Pro Gln Phe Tyr Pro Leu Lys
 130 135 140
 Lys Gly Tyr Tyr Thr His Ile Thr Tyr Asn Asp Asp Ser Met Val Asn
 145 150 155 160
 Ile Leu Met Ile Leu Lys Asn Ile Lys Glu Asp Ala Asn Tyr Tyr Ser
 165 170 175
 Ile Thr Pro Ser Asp Lys Val Leu Lys Gln Val Ser Thr Ala Phe Asp
 180 185 190
 Arg Gly Ile Asp Cys Ile Leu Lys Thr Gln Tyr Lys Gln Lys Gly Val
 195 200 205
 Leu Thr Ser Trp Cys Ala Gln His Asp Glu Val Thr Leu Glu Pro Ala
 210 215 220
 Asn Ala Arg Ala Phe Glu Leu Ala Ser Leu Ser Gly Lys Glu Ser Ala
 225 230 235 240
 Lys Ile Thr Leu Leu Leu Met Ser Val Lys Asn Pro Ser Lys Glu Val
 245 250 255
 Val Ala Ala Val Asp Ala Ala Val Ala Trp Phe Glu Lys Thr Lys Ile
 260 265 270
 Glu Gly Ile Lys Val Glu Glu Val Thr Gly Ala Asp Gly Lys Lys Asp
 275 280 285
 Arg Val Val Val Gln Arg Ala Asp Ala Glu Pro Leu Trp Ala Arg Phe
 290 295 300
 Met Glu Leu Asp Thr Asn Arg Pro Phe Phe Cys Asp Arg Asp Gly Ile
 305 310 315 320
 Lys Lys Tyr Ser Leu Ala Glu Ile Gly His Glu Arg Arg Asn Gly Tyr
 325 330 335
 Gly Trp Tyr Thr Asn Glu Pro Lys Glu Val Leu Lys Lys Tyr Thr Lys
 340 345 350
 Trp Lys Asn Ser Leu Lys
 355

<210> 49

<211> 1023

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 49

atgttaagtt	tcacgcggt	atcagtgttt	cataattact	gcacagggca	gacagcgtcc	60
accaaaaatt	cagtggccga	aaagatgctt	cagtaccagt	tgtcaaattg	cgccctggccc	120
aaacagttgg	tagacaaaag	tgctgttgat	tacagtcttc	cattaacgaa	agagcgccta	180
cagcagatca	agaaaacaga	tattgatcat	gctacgctcg	acaacagtgc	gacaacccgg	240
gaaataactg	aattgatcaa	ggcttttaag	gacactaaaa	ataaggcata	tttgactgct	300
gtagaaaagg	ggattgcata	tattttatcg	gctcaatatg	agaatggcgg	atttccacaa	360
tactacccaa	ataaattata	ctatagagct	gagataacat	acaacgatga	tgcgatgatc	420
aatgcattac	tagtgcttta	caaagtagcc	aataagcgag	aggggtttga	ggctatcaat	480
cccatatttg	tgtcaaaagc	gcaaaaagca	gttgaaaagg	gtataacctg	tatcctaata	540
acacagggtca	tacaagacgg	aaaaaggagt	atttgggctg	cgcaatacga	tcagaacact	600
ttacaacctg	ctcaggcaag	aaagtttgaa	ccagcttcat	tgagcacaag	tgaatctgtt	660
tcacatcggt	gctttctcat	gctacagcct	gcaaccactg	aaattaagca	agcgatcgaa	720
catgcaatac	aatgggtcga	acagcatgat	attgaagggt	accgtttcga	ccgcatacaa	780
gatagggtga	ctggaaaata	tcaacggcaa	cttgctgcag	atcggacttc	cacgatttgg	840
gcgcgatttt	ataatctcga	agacaaccgc	ccattgtttg	gagatcgggg	caatacaatc	900
aaatacaact	ttgaggaggt	ttcagaggag	cgtagaaatg	gctatgcttg	gttcggcaac	960
tggccggaaa	agctgatcca	aaaggactat	ccaaaatgga	aaaaacaata	caaaattaaa	1020

taa

1023

<210> 50
 <211> 340
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(16)

<221> DOMAIN
 <222> (17)...(340)
 <223> Catalytic domain

<400> 50
 Met Leu Ser Phe Ile Ala Val Ser Val Phe His Asn Tyr Cys Thr Gly
 1 5 10 15
 Gln Thr Ala Ser Thr Lys Asn Ser Val Ala Glu Lys Met Leu Gln Tyr
 20 25 30
 Gln Leu Ser Asn Gly Ala Trp Pro Lys Gln Leu Val Asp Lys Ser Val
 35 40 45
 Val Asp Tyr Ser Leu Pro Leu Thr Lys Glu Arg Leu Gln Gln Ile Lys
 50 55 60
 Lys Thr Asp Ile Asp His Ala Thr Leu Asp Asn Ser Ala Thr Thr Arg
 65 70 75 80
 Glu Ile Thr Glu Leu Ile Lys Ala Phe Lys Asp Thr Lys Asn Lys Ala
 85 90 95
 Tyr Leu Thr Ala Val Glu Lys Gly Ile Ala Tyr Ile Leu Ser Ala Gln
 100 105 110
 Tyr Glu Asn Gly Gly Phe Pro Gln Tyr Tyr Pro Asn Lys Leu Tyr Tyr
 115 120 125
 Arg Ala Glu Ile Thr Tyr Asn Asp Asp Ala Met Ile Asn Ala Leu Leu
 130 135 140
 Val Leu Tyr Lys Val Ala Asn Lys Arg Glu Gly Phe Glu Ala Ile Asn
 145 150 155 160
 Pro Ile Phe Val Ser Lys Ala Gln Lys Ala Val Glu Lys Gly Ile Thr
 165 170 175
 Cys Ile Leu Lys Thr Gln Val Ile Gln Asp Gly Lys Arg Ser Ile Trp
 180 185 190
 Ala Ala Gln Tyr Asp Gln Asn Thr Leu Gln Pro Ala Gln Ala Arg Lys
 195 200 205
 Phe Glu Pro Ala Ser Leu Ser Thr Ser Glu Ser Val Ser Ile Val Arg
 210 215 220
 Phe Leu Met Leu Gln Pro Ala Thr Thr Glu Ile Lys Gln Ala Ile Glu
 225 230 235 240
 His Ala Ile Gln Trp Phe Glu Gln His Asp Ile Glu Gly Tyr Arg Phe
 245 250 255
 Asp Arg Ile Gln Asp Arg Val Thr Gly Lys Tyr Gln Arg Gln Leu Val
 260 265 270
 Ala Asp Arg Thr Ser Thr Ile Trp Ala Arg Phe Tyr Asn Leu Glu Asp
 275 280 285
 Asn Arg Pro Leu Phe Gly Asp Arg Asp Asn Thr Ile Lys Tyr Asn Phe
 290 295 300
 Glu Glu Val Ser Glu Glu Arg Arg Asn Gly Tyr Ala Trp Phe Gly Asn
 305 310 315 320
 Trp Pro Glu Lys Leu Ile Gln Lys Asp Tyr Pro Lys Trp Lys Lys Gln

Tyr Lys Ile Lys
340

325

330

335

<210> 51
<211> 1131
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 51
gtgacgtggg atcagatcct tcgtcagcct gccgcctggt acggcgggtcc ggaagcgcga 60
cggatcgcga atctggtcct gctgtaccag cgcgcgacgg ggggctggcc caagaacatc 120
gacatggcgc ggtcgtttgtc tccggacgat cgcacgacgc tcgcggcgga acggggccctc 180
accgactcga cgatcgacaa tggatcgacg acgacgcagt tgcggtttct cgcgatgggtg 240
cagcacgccc agcaggcacc cgtgcgcgac gccatcacgc acggcctgga ctatctgctg 300
aacgcgcaat actcgaacgg cggatggccg cagtactttc cgctccgaga cgactactcg 360
cgtcacatca cgttcaacga cgacgcgatg atcaatgtaa tgacgggtgct acgcgatgtc 420
gcagaagctc gcatgccctt cgaagggatc gacgcgggtcc gtcgggaccg ggcgcggtgc 480
gccatcacgc gtggcatcga cgtgattctc gggacgcaaa tccgcgtcgg ggaccgtctg 540
acgggctggt gccagcagca tgacgagcgc tccctcgccc ccaccaaggc tcgcgcctac 600
gagcacccat cgatcgccag caaggaaacg gtaaccatca cgcgcttcct catgaccctc 660
gatcgcccga gtcagcagat catcgcgggc atcgaggcgg ctgtcgagtg gttgcgcgtg 720
gcgaccctgt cgggtgtgcg agttgagcgt cggccggacc cggcgagtcc gaccggatat 780
gacgtcgtcg ccgcgccgga tgccgcgcga cctccgacct gggcacgggt ctacgagatc 840
ggcagaacc gccaatggt ttccggccgc gacggcgtga tcagattccg gctcgcggac 900
atcgagattg agcgcgcgac cggctacagc tggatgggcg actatgccgc gaggttgctg 960
aacgaggagt atccggcgtg ggcgaggcta cgccgggcga gctttcagaa cgccgagctg 1020
cacaaggagt ccggtgaagt cgtacacacg gcgatcgtgc acgatcttgc cttccttgat 1080
gtcgaagaca aagaccagcc gcagccgaaa gtgcttttcg ctgggcggta g 1131

<210> 52
<211> 376
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(376)
<223> Catalytic domain

<400> 52
Met Thr Trp Asp Gln Ile Leu Arg Gln Pro Ala Ala Trp Tyr Gly Gly
1 5 10 15
Pro Glu Ala Arg Ile Ala Asn Leu Val Leu Leu Tyr Gln Arg Ala
20 25 30
Thr Gly Gly Trp Pro Lys Asn Ile Asp Met Ala Arg Ser Leu Ser Pro
35 40 45
Asp Asp Arg Thr Thr Leu Ala Ala Glu Arg Ala Leu Thr Asp Ser Thr
50 55 60
Ile Asp Asn Gly Ser Thr Thr Thr Gln Leu Arg Phe Leu Ala Met Val
65 70 75 80
Gln His Ala Gln Gln Ala Pro Val Arg Asp Ala Ile Thr His Gly Leu
85 90 95
Asp Tyr Leu Leu Asn Ala Gln Tyr Ser Asn Gly Gly Trp Pro Gln Tyr

[illegible]

<210>	53
<211>	1977
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<400>	53						
atgaataact	caacaaaaaa	aatgattcgg	ccactcaagg	catcttttgc	cttgggcgct		60
ctcgcaactg	caatcgcatc	accctcatgg	gcggcttgct	cttacagcgt	aaccaataat		120
tggggctctg	gctttaccgg	agaaattaaa	gtaaccaacg	atacaacatc	gactgtaaat		180
aattggtctg	tgtcttggca	ggaatcaggc	gtgaccgtca	ctaacgcgtg	gactgcaaca		240
ctgagcggat	caaatctcta	taccgcaaca	tcactcgggt	ggaacggaac	tctcgctcca		300
aaagcttcag	caagttttgg	ttttcaagca	aatggaacag	cgggcgcacc	gaaagtaaat		360
ggaaccttgt	gtggtaccag	cacatcatca	acaggtacat	cctcagttgc	accttcatcc		420
gtagcgagta	gcgttgctgt	atcaagcagt	aaatcatcaa	gctctgttgc	aaccatcagt		480
agctctaaat	ccagcagcag	tgtgccgaca	gtttcatcat	tcactattca	ggaagagcaa		540
gccggtttct	gccgtgtaga	tggcattgca	actgaaagta	ctaacactgg	ctatacaggt		600
aatggctaca	ccaacaccac	taatgcgcaa	ggcgtgcgaa	ttgaatgggc	acctaatgct		660
cccaacagca	gccgtatac	ctcaccttct	cgttatgcc	atgctggatc	cgttaattgc		720
aatggttcgt	tattataatt	cgacggaagc	aatggtaact	acacagtgca	attgccaaagt		780
accggcgcat	gggcaacctg	gcaaacctgc	agtgttgaag	tggatttggt	gcaaggcaat		840

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aatattttga aactcgcttc gcttactgct gatggccttg cgaatataga ttcattaaaa 900
attgaaggcg cacaagccaa agctggtgta tgcagcacta cggtaagtag cagctcttcg 960
tcaattaaat caagttccag ttcattcatcg tccagctcaa ctgcagcagt aaaaacatta 1020
acactggatg gtaaccctgc tgcaaaactg ttaataaat ccagaaccaa gtggaatgtc 1080
agcagagctg acatcgctt ttcgtatcag caatcaaagtg gtggctggcc aaaaaatttg 1140
gactacaact cggtaggctc aggtaatggt ggtagcgaca gcggcactat tgataatggt 1200
gcaaccataa ccgaaatggt gtacctcgct gaagtgtata aaaatggcgg gaataccaaa 1260
taccgcgacg ccgtgcgcag agcagcgaat tttattgtga gttcacaata cagcactggt 1320
gctttaccgc agttttatcc gctgaaaggt ggttacgcag atcacgctac ctttaatgat 1380
aatggtatgg cttacgcggt gactgttctg gatttcgcgg taaataaacg cgcgccattt 1440
gataacgata ttttctctga ctctgaccgc agcaaattta aaactgctgt taccaaaggc 1500
gtcgattaca tattaanaagc gcaatggaaa cagaatggaa aattaaccgt atggtgcgca 1560
caacacggtg ctaatgatta tcaaccgaaa aaagcgcgtg cttacgagtt agaattcattg 1620
agtggtagtg aatctgtcgg tgtactcgct ttcttaatga ctcaaccaca aaccacgcaa 1680
attgaagcag ctgtgcgtgc aggtgtggcc tggtttaata gcccaagcac ctacttgaat 1740
aattacactt acgattcttc caaagcttcg accaatccaa tcgtgccaaa atccggaagc 1800
aaaatgtggt atcgctttta tgacctgaat accaaccgcg gtttcttcag tgatcgtgac 1860
ggcagcaagt tctacgacat caccctaaatg tcagaagagc gtcgcactgg ttacagttgg 1920
ggtggtgact acggcagctc gattatcagc ttcgcacaaa aagtgggata tctctaa 1977

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<210> 54
 <211> 658
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(31)

<221> BINDING
 <222> (32)...(124)
 <223> Carbohydrate binding module

<221> BINDING
 <222> (180)...(303)
 <223> Carbohydrate binding module

<221> DOMAIN
 <222> (304)...(658)
 <223> Catalytic domain

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<400> 54
Met Asn Asn Ser Thr Lys Lys Met Ile Arg Pro Leu Lys Ala Ser Phe
 1             5             10             15
Ala Leu Gly Ala Leu Ala Leu Ala Ile Ala Ser Pro Ser Trp Ala Ala
 20             25             30
Cys Ser Tyr Ser Val Thr Asn Asn Trp Gly Ser Gly Phe Thr Gly Glu
 35             40             45
Ile Lys Val Thr Asn Asp Thr Thr Ser Thr Val Asn Asn Trp Ser Val
 50             55             60
Ser Trp Gln Glu Ser Gly Val Thr Val Thr Asn Ala Trp Asn Ala Thr
 65             70             75             80
Leu Ser Gly Ser Asn Pro Tyr Thr Ala Thr Ser Leu Gly Trp Asn Gly
 85             90             95
Thr Leu Ala Pro Lys Ala Ser Ala Ser Phe Gly Phe Gln Ala Asn Gly
100            105            110
Thr Ala Gly Ala Pro Lys Val Asn Gly Thr Leu Cys Gly Thr Ser Thr

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115	120	125
Ser Ser Thr Gly Thr Ser Ser	Val Ala Pro Ser Ser	Val Ala Ser Ser
130	135	140
Val Ala Val Ser Ser Ser	Lys Ser Ser Ser	Val Ala Thr Ile Ser
145	150	155
Ser Ser Lys Ser Ser Ser	Val Pro Thr Val Ser Ser	Phe Thr Ile
165	170	175
Gln Glu Glu Gln Ala Gly Phe	Cys Arg Val Asp Gly Ile Ala Thr Glu	
180	185	190
Ser Thr Asn Thr Gly Tyr Thr	Gly Asn Gly Tyr Thr Asn Thr Thr Asn	
195	200	205
Ala Gln Gly Ala Ala Ile Glu	Trp Ala Ile Asn Ala Pro Asn Ser Ser	
210	215	220
Arg Tyr Thr Leu Thr Phe Arg	Tyr Ala Asn Ala Gly Thr Ala Asn Arg	
225	230	235
Asn Gly Ser Leu Leu Ile Asn	Asp Gly Ser Asn Gly Asn Tyr Thr Val	
245	250	255
Gln Leu Pro Ser Thr Gly Ala	Trp Ala Thr Trp Gln Thr Val Ser Val	
260	265	270
Glu Val Asp Leu Val Gln Gly	Asn Ile Leu Lys Leu Ala Ser Leu	
275	280	285
Thr Ala Asp Gly Leu Ala Asn	Ile Asp Ser Leu Lys Ile Glu Gly Ala	
290	295	300
Gln Ala Lys Ala Gly Val Cys	Ser Thr Thr Val Ser Ser Ser Ser	
305	310	315
Ser Ile Lys Ser Ser Ser Ser	Ser Ser Ser Ser Thr Ala Ala	
325	330	335
Val Lys Thr Leu Thr Leu Asp	Gly Asn Pro Ala Ala Asn Trp Phe Asn	
340	345	350
Lys Ser Arg Thr Lys Trp Asn	Val Ser Arg Ala Asp Ile Val Leu Ser	
355	360	365
Tyr Gln Gln Ser Asn Gly Gly	Trp Pro Lys Asn Leu Asp Tyr Asn Ser	
370	375	380
Val Gly Ser Gly Asn Gly Gly	Ser Asp Ser Gly Thr Ile Asp Asn Gly	
385	390	395
Ala Thr Ile Thr Glu Met Val	Tyr Leu Ala Glu Val Tyr Lys Asn Gly	
405	410	415
Gly Asn Thr Lys Tyr Arg Asp	Ala Val Arg Arg Ala Ala Asn Phe Ile	
420	425	430
Val Ser Ser Gln Tyr Ser Thr	Gly Ala Leu Pro Gln Phe Tyr Pro Leu	
435	440	445
Lys Gly Gly Tyr Ala Asp His	Ala Thr Phe Asn Asp Asn Gly Met Ala	
450	455	460
Tyr Ala Leu Thr Val Leu Asp	Phe Ala Val Asn Lys Arg Ala Pro Phe	
465	470	475
Asp Asn Asp Ile Phe Ser Asp	Ser Asp Arg Ser Lys Phe Lys Thr Ala	
485	490	495
Val Thr Lys Gly Val Asp Tyr	Ile Leu Lys Ala Gln Trp Lys Gln Asn	
500	505	510
Gly Lys Leu Thr Val Trp Cys	Ala Gln His Gly Ala Asn Asp Tyr Gln	
515	520	525
Pro Lys Lys Ala Arg Ala Tyr	Glu Leu Glu Ser Leu Ser Gly Ser Glu	
530	535	540
Ser Val Gly Val Leu Ala Phe	Leu Met Thr Gln Pro Gln Thr Thr Gln	
545	550	555
Ile Glu Ala Ala Val Arg Ala	Gly Val Ala Trp Phe Asn Ser Pro Ser	
565	570	575
Thr Tyr Leu Asn Asn Tyr Thr	Tyr Asp Ser Ser Lys Ala Ser Thr Asn	
580	585	590

Pro Ile Val Pro Lys Ser Gly Ser Lys Met Trp Tyr Arg Phe Tyr Asp
 595 600 605
 Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp Arg Asp Gly Ser Lys Phe
 610 615 620
 Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg Thr Gly Tyr Ser Trp
 625 630 635 640
 Gly Gly Asp Tyr Gly Ser Ser Ile Ile Ser Phe Ala Gln Lys Val Gly
 645 650 655
 Tyr Leu

<210> 55
 <211> 1125
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 55
 gtggtcctag gtaataacgg cggcagcttg agttgctgcc aatatattgt gattgtgaaa 60
 ggacccggtg gacctcgacc gccggtgaaa ccggccgtcc aggcgcccgt tagggttacc 120
 tggagcgcac gcctagtcca gcggcccga tggtagcgga gtgacgaagc gatccgcac 180
 gcggacaacg tcctctctta ccagcgcaac accggcgggt ggccgaagga catagatatg 240
 gccgagccca tcccgaaca caggaagtcc tttttcctca ccgagaagga gcggaccgat 300
 gactcgacca tcgacaacgg tgccaccgtg acccagctca agtatctcgc ccgcgtctac 360
 aaggcgacca ggctggaacg gttcaaggag ggcttcctca aagggtctcga ctacctcttg 420
 gccgcccagt acccgaacgg cggctggccc cagtattatc ctaacttgag gggctactac 480
 gccaacatca cttataacga caatgccatg gtgaacgtgc tcaccctcct ccagagcatc 540
 gccaaaaagg ccccgagta cgacttcgtc gaccggcgc gccgggagaa ggccgcccgg 600
 gccgtggcga aagggatcga ctgcatcctc aagaccaga tccgtgtcaa tggaaaactt 660
 accgcctggt gcgcccagca tgaccccaag acgctggcgc ccgcgccggc ccgttcgtat 720
 gagcttgagt ccatcagcgg tttcgagagc gtcgggatcg tccggttctt aatgagcctc 780
 gagaatccga gcccggaagg catcgaggcg gtagaggccg ccgtgaaatg gtccgaggag 840
 gtcaagctta ccgggatcaa ggtggtcgag aaaccggacc cgtcccttcc gggcggttac 900
 gaccgcgtgg tggtcgaaga cccaacgcg ccgcccatct gggcccgggt ctacgagatc 960
 ggcaccaacc gtcccttctt ctgcggccgc gatggtatca aaaaatacag cctggcggag 1020
 atcgaacacg aacgccgggt cggttactcc tggtaacca atgccccggc ctacctcatc 1080
 gagaaggagt atccgctctg gcgggccaaa caccctacca agtaa 1125

<210> 56
 <211> 374
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(374)
 <223> Catalytic domain

<400> 56
 Met Val Leu Gly Asn Asn Gly Gly Ser Leu Ser Cys Val Gln Tyr Ile
 1 5 10 15
 Val Ile Val Lys Gly Pro Gly Gly Pro Arg Pro Pro Val Lys Pro Ala
 20 25 30
 Val Gln Ala Pro Val Arg Val Thr Trp Ser Ala Cys Leu Val Gln Arg
 35 40 45

Pro	Glu	Trp	Tyr	Gly	Ser	Asp	Glu	Ala	Ile	Arg	Ile	Ala	Asp	Asn	Val
50						55					60				
Leu	Leu	Tyr	Gln	Arg	Asn	Thr	Gly	Gly	Trp	Pro	Lys	Asp	Ile	Asp	Met
65					70					75					80
Ala	Glu	Pro	Ile	Pro	Glu	His	Arg	Lys	Ser	Phe	Phe	Leu	Thr	Glu	Lys
				85					90					95	
Glu	Arg	Thr	Asp	Asp	Ser	Thr	Ile	Asp	Asn	Gly	Ala	Thr	Val	Thr	Gln
			100					105					110		
Leu	Lys	Tyr	Leu	Ala	Arg	Val	Tyr	Lys	Ala	Thr	Arg	Leu	Glu	Arg	Phe
	115						120					125			
Lys	Glu	Gly	Phe	Leu	Lys	Gly	Leu	Asp	Tyr	Leu	Leu	Ala	Ala	Gln	Tyr
	130					135						140			
Pro	Asn	Gly	Gly	Trp	Pro	Gln	Tyr	Tyr	Pro	Asn	Leu	Arg	Gly	Tyr	Tyr
145					150					155					160
Ala	Asn	Ile	Thr	Tyr	Asn	Asp	Asn	Ala	Met	Val	Asn	Val	Leu	Thr	Leu
			165						170					175	
Leu	Gln	Ser	Ile	Ala	Lys	Lys	Ala	Pro	Glu	Tyr	Asp	Phe	Val	Asp	Pro
		180					185						190		
Ala	Arg	Arg	Glu	Lys	Ala	Ala	Arg	Ala	Val	Ala	Lys	Gly	Ile	Asp	Cys
	195						200					205			
Ile	Leu	Lys	Thr	Gln	Ile	Arg	Val	Asn	Gly	Lys	Leu	Thr	Ala	Trp	Cys
	210					215						220			
Ala	Gln	His	Asp	Pro	Lys	Thr	Leu	Ala	Pro	Ala	Pro	Ala	Arg	Ser	Tyr
225					230					235					240
Glu	Leu	Glu	Ser	Ile	Ser	Gly	Phe	Glu	Ser	Val	Gly	Ile	Val	Arg	Phe
			245						250					255	
Leu	Met	Ser	Leu	Glu	Asn	Pro	Ser	Pro	Lys	Val	Ile	Glu	Ala	Val	Glu
		260						265					270		
Ala	Ala	Val	Lys	Trp	Phe	Glu	Glu	Val	Lys	Leu	Thr	Gly	Ile	Lys	Val
	275						280					285			
Val	Glu	Lys	Pro	Asp	Pro	Ser	Leu	Pro	Gly	Gly	Tyr	Asp	Arg	Val	Val
	290					295					300				
Val	Glu	Asp	Pro	Asn	Ala	Pro	Pro	Ile	Trp	Ala	Arg	Phe	Tyr	Glu	Ile
305					310					315					320
Gly	Thr	Asn	Arg	Pro	Phe	Phe	Cys	Gly	Arg	Asp	Gly	Ile	Lys	Lys	Tyr
			325						330					335	
Ser	Leu	Ala	Glu	Ile	Glu	His	Glu	Arg	Arg	Val	Gly	Tyr	Ser	Trp	Tyr
		340					345						350		
Thr	Asn	Ala	Pro	Ala	Tyr	Leu	Ile	Glu	Lys	Glu	Tyr	Pro	Leu	Trp	Arg
	355						360						365		
Ala	Lys	His	Pro	Thr	Lys										
	370														

<210> 57

<211> 1170

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 57

atggacaaac	gcgtcaaatg	gattcatcag	ctttcaaaag	aagaagcaaa	gcagttcgag	60
cccgaaaatt	tcctcaaagg	caaagacggc	tggaatccga	aaaaggcgga	tgaccgctgg	120
ctcgaaaaaa	caaaacctga	ctggcagctc	gttacgtgga	acgacgcgtt	acgccaggcg	180
ccgctctggt	atcaaaccga	tgaagcggcg	cgcattgccg	accaggtgat	tttgtaccag	240
aaagacaacg	gcggctggga	aaaaaatctc	gatatgacgg	cgatgctcac	gcaagccgaa	300
cgcgaaaagc	tcgccaaaga	aaaatcgaac	acgtcggaac	cgacgatcga	caaccgcacg	360
acctacacgc	aagtcgcttt	tctcgccaaa	gtcattacgg	gcagcttgca	gaaaacgact	420

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ccgccgacca atttcccga acataaggaa gcttttttca agggccttga ttacctgctc 480
gcgtcgcagt acgaatcggg cggcttttccg cagtttttacc cgtcaaaaaa aggttattac 540
acgcacatca cgttcaacga cgatgcgatg attggcggtt tgaagggttt gcgcgaaatc 600
gccaaaaaga aggaagacta tctttttgtt gacgaagaac gccgcctgaa agcggaaaaa 660
tcggtcgaaa aagcgctgcc gctgattctg aaattgcagg ttgaagtcgg cggcaaaaaa 720
acggttttgg cggcgagta tgacgaaaac acttttaaac ccgcagcggc gcgaaagtgt 780
gaaccgggtt ctttaacggc gggcgaaatc gtcggcatcg tccggttttt aatgtacgat 840
tcaaagcccg accagcgac gattgacgag attgaatctg ccattcagtg gtatcgcgcg 900
aacaaaatcg aaggcattcg atgggtgcgc gaaaacggcg aaaaccgcgt cgtcaaggac 960
aaaaacgcgc cggcgatttg ggcgcggttt tacgaaatcg aaacgatgaa gccgattttc 1020
atcgggcgcg acgccatcat tcgttacgac gtgtctgaaa tcgaagccga gcgccgcaac 1080
ggctacgcgt ggtacgtctc ggagccgaac gagctgcttg aaaaagatta cccgaaatgg 1140
ctggaaaaaa ttaaaaaatc agtaaagtaa 1170

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<210> 58
 <211> 389
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(389)
 <223> Catalytic domain

<400> 58

Met	Asp	Lys	Arg	Val	Lys	Trp	Ile	His	Gln	Leu	Ser	Lys	Glu	Glu	Ala
1				5					10				15		
Lys	Gln	Phe	Glu	Pro	Glu	Asn	Phe	Leu	Lys	Gly	Lys	Asp	Gly	Trp	Asn
			20					25					30		
Pro	Lys	Lys	Ala	Asp	Asp	Arg	Trp	Leu	Glu	Lys	Thr	Lys	Pro	Asp	Trp
			35				40					45			
Gln	Leu	Val	Thr	Trp	Asn	Asp	Ala	Leu	Arg	Gln	Ala	Pro	Leu	Trp	Tyr
	50				55					60					
Gln	Thr	Asp	Glu	Ala	Ala	Arg	Ile	Ala	Asp	Gln	Val	Ile	Leu	Tyr	Gln
65					70				75					80	
Lys	Asp	Asn	Gly	Gly	Trp	Glu	Lys	Asn	Leu	Asp	Met	Thr	Ala	Met	Leu
			85					90					95		
Thr	Gln	Ala	Glu	Arg	Glu	Lys	Leu	Ala	Lys	Glu	Lys	Ser	Asn	Thr	Ser
			100					105					110		
Glu	Thr	Thr	Ile	Asp	Asn	Arg	Thr	Tyr	Thr	Gln	Val	Ala	Phe	Leu	
			115				120					125			
Ala	Lys	Val	Ile	Thr	Gly	Ser	Leu	Gln	Lys	Thr	Thr	Pro	Pro	Thr	Asn
			130			135					140				
Phe	Pro	Lys	His	Lys	Glu	Ala	Phe	Phe	Lys	Gly	Leu	Asp	Tyr	Leu	Leu
145					150				155					160	
Ala	Ser	Gln	Tyr	Glu	Ser	Gly	Gly	Phe	Pro	Gln	Phe	Tyr	Pro	Leu	Lys
			165					170						175	
Lys	Gly	Tyr	Tyr	Thr	His	Ile	Thr	Phe	Asn	Asp	Asp	Ala	Met	Ile	Gly
			180				185					190			
Val	Leu	Lys	Val	Leu	Arg	Glu	Ile	Ala	Lys	Lys	Lys	Glu	Asp	Tyr	Leu
			195			200						205			
Phe	Val	Asp	Glu	Glu	Arg	Arg	Leu	Lys	Ala	Glu	Lys	Ser	Val	Glu	Lys
			210			215					220				
Ala	Leu	Pro	Leu	Ile	Leu	Lys	Leu	Gln	Val	Glu	Val	Gly	Gly	Lys	Lys
225					230				235					240	
Thr	Val	Trp	Ala	Ala	Gln	Tyr	Asp	Glu	Asn	Thr	Phe	Lys	Pro	Ala	Ala
			245					250						255	

Ala	Arg	Lys	Phe	Glu	Pro	Val	Ser	Leu	Thr	Ala	Gly	Glu	Ser	Val	Gly
			260					265					270		
Ile	Val	Arg	Phe	Leu	Met	Tyr	Asp	Ser	Lys	Pro	Asp	Gln	Ala	Thr	Ile
		275					280					285			
Asp	Ala	Ile	Glu	Ser	Ala	Ile	Gln	Trp	Tyr	Arg	Ala	Asn	Lys	Ile	Glu
		290				295					300				
Gly	Ile	Arg	Trp	Val	Arg	Glu	Asn	Gly	Glu	Asn	Arg	Val	Val	Lys	Asp
305					310				315					320	
Lys	Asn	Ala	Pro	Pro	Ile	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Glu	Thr	Met
				325					330					335	
Lys	Pro	Ile	Phe	Ile	Gly	Arg	Asp	Ala	Ile	Ile	Arg	Tyr	Asp	Val	Ser
			340					345					350		
Glu	Ile	Glu	Ala	Glu	Arg	Arg	Asn	Gly	Tyr	Ala	Trp	Tyr	Val	Ser	Glu
		355					360					365			
Pro	Asn	Glu	Leu	Leu	Glu	Lys	Asp	Tyr	Pro	Lys	Trp	Leu	Glu	Lys	Ile
	370					375					380				
Lys	Lys	Ser	Val	Lys											
385															

<210> 59
 <211> 1080
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 59	
atgagaatcc ggtcctcttc aatcgcgttc ggcctgattt gcagtctggc gctaaggggtg	60
cctgcgcaag cgcaggtcac cgtgcgctgg gcgacgtcc tgaaccagcc cgccgcctgg	120
tatggcaccg atgaagcccg tcgaattgcc gaccacgtgc tcgagcatca acgagcggaa	180
ggcggatggc caaagaacac ggacatgacc gcagcgcccg atccggcggt gctcacagcc	240
gcgcgagtga agccagactc gacgatcgat aacggcgcgga ccgtcactga aatgcgcgtc	300
ctcgcgcgcg tctaccgttc atcaccggat ccccgttatc gcgatgcgct gctcaaggggt	360
ctcgactatc tgttggcagc gcagtatgcc aacggcggtt ggccgcagtt ctaccgcgtc	420
cggcaggact attcgcgcta tatcacgttc aacgacaacg cgatgatcaa tgtcgtgacg	480
ctgctctcag acgtcgcgtc cggaaatggc gactgggctt ttgctgatgc cagccggcgc	540
gagaaaagcc ggacggctgt agagaaggcc gtagaagtca tctgcgcgc gcaggtgaga	600
gttgacggcc ggctgacgc gtggtgcgcc caacacgacg aggtgacact cgagccgcgc	660
aaggcccgcg cctacgaaca tccgtcgctg agcggacagg agacgggtggg gatcatccgg	720
tttctcatga cccgcgataa accggatcag agagtcgtcg atgcaatcga ggcgtcagtg	780
gcatggctga aggcggtgca gctcaaagga cttcgcgtcg accagcgccg cgatccctcg	840
ctgccggagg ggcgtgacgt ggtgaccgtc gctgaccggt cggcgccgcc gctctgggcg	900
cgcttctacg aaatcgggac caatcgcgcc atcttctctg gacgcgacgg cgtgatccga	960
tactcgctgg cagagatcga gcacgaacgc cggatagggt acgcctggct cggaacctgg	1020
cccgcgaagc tgctcgatac cgaataccca tcttgccgac ggactcaaca aaggccgtga	1080

<210> 60
 <211> 359
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(24)

<221> DOMAIN

<222> (25)...(359)

<223> Catalytic domain

<400> 60

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Met Arg Ile Arg Ser Ser Ser Ile Ala Phe Gly Leu Ile Cys Ser Leu
 1           5           10
Ala Leu Arg Val Pro Ala Gln Ala Gln Val Thr Val Arg Trp Ala Asp
          20           25           30
Val Leu Asn Gln Pro Ala Ala Trp Tyr Gly Thr Asp Glu Ala Arg Arg
          35           40           45
Ile Ala Asp His Val Leu Glu His Gln Arg Ala Glu Gly Gly Trp Pro
          50           55           60
Lys Asn Thr Asp Met Thr Ala Ala Pro Asp Pro Ala Val Leu Thr Ala
65           70           75           80
Ala Arg Val Lys Pro Asp Ser Thr Ile Asp Asn Gly Ala Thr Val Thr
          85           90           95
Glu Met Arg Val Leu Ala Arg Val Tyr Arg Ser Ser Pro Asp Pro Arg
          100          105          110
Tyr Arg Asp Ala Leu Leu Lys Gly Leu Asp Tyr Leu Leu Ala Ala Gln
          115          120          125
Tyr Ala Asn Gly Gly Trp Pro Gln Phe Tyr Pro Leu Arg Gln Asp Tyr
          130          135          140
Ser Arg Tyr Ile Thr Phe Asn Asp Asn Ala Met Ile Asn Val Val Thr
145          150          155          160
Leu Leu Ser Asp Val Ala Ala Gly Asn Gly Asp Trp Ala Phe Ala Asp
          165          170          175
Ala Ser Arg Arg Glu Lys Ser Arg Thr Ala Val Glu Lys Ala Val Glu
          180          185          190
Val Ile Leu Arg Ala Gln Val Arg Val Asp Gly Arg Leu Thr Ala Trp
          195          200          205
Cys Ala Gln His Asp Glu Val Thr Leu Glu Pro Arg Lys Ala Arg Ala
210          215          220
Tyr Glu His Pro Ser Leu Ser Gly Gln Glu Thr Val Gly Ile Ile Arg
225          230          235          240
Phe Leu Met Thr Arg Asp Lys Pro Asp Gln Arg Val Val Asp Ala Ile
          245          250          255
Glu Ala Ser Val Ala Trp Leu Lys Ala Val Gln Leu Lys Gly Leu Arg
          260          265          270
Val Asp Gln Arg Arg Asp Pro Ser Leu Pro Glu Gly Arg Asp Val Val
          275          280          285
Thr Val Ala Asp Pro Ser Ala Pro Pro Leu Trp Ala Arg Phe Tyr Glu
          290          295          300
Ile Gly Thr Asn Arg Pro Ile Phe Ser Gly Arg Asp Gly Val Ile Arg
305          310          315          320
Tyr Ser Leu Ala Glu Ile Glu His Glu Arg Arg Ile Gly Tyr Ala Trp
          325          330          335
Leu Gly Thr Trp Pro Ala Lys Leu Leu Asp Thr Glu Tyr Pro Ser Trp
          340          345          350
Arg Arg Thr Gln Gln Arg Pro
          355

```

<210> 61

<211> 1224

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

```

<400> 61
gtggaattac cagtaaccgg cgcattgggca acctggcaaa ccgcaactgt tgaaattgat      60
tttgtgcaag gtaacaacct gttaaaactt tctgcgatca cggctgatgg ttgggcaaatt      120
atcgattcgt tgaaaattga cggcgacaaa accaaagccg gcgtgtgcag cactgtggca      180
agcagcagct cttcatccgt tgcttcatcg attaaatcaa gctccagttc atcctcttcc      240
agttcaacga cgacggtaaa aacattaaca ctggatggca accccgcagc aaactggttt      300
aacaaatcca gaaccaaatg gaataaccagc agagccgatg ttgtactttc ctatcaacaa      360
tccaacggcg gctggccaaa aaatctcgat tacaattcag taagcgcagg taatggcggc      420
agcgatagcg gcaccatcga taacggtgca accattactg aaatggttta tctcgcggaa      480
gtttacaaaa atggcaacaa caccaagtat cgcgatgcgg tgcgagagc cgcaaatttt      540
attgtcagct cgcaatacag cactggtgca ttaccacaat tttatccatt gaaaggcggc      600
tatgcagacc acgccacctt taacgataac ggcattggat atgcattaac ggtattggat      660
tttgagtcga acaaacgcgc cccatttgat actgatgttt tctccgattc tgatcgcgcg      720
aaattcaaaa ccgctgtgtg caaagggtgtg gattacattt tgaaagcgca gtggaaacaa      780
aacggaaaat taaccgtgtg gtgtgcacaa catggtgcta ccgattatca accgaaaaaa      840
gcgcgcgcct atgaattgga atcactgagt ggcagcgaat ctggtgggtg actcgttttc      900
ttgatgacct aaccgcaaac cgcacaaatt gaagccgctg taaaagccgg tgtagcctgg      960
ttcaatagcc ccaacacgta tttgaacaat tacacttacg actcttcaaa agcgtcaact     1020
aatccaatag ttgccaagtc tggaagcaaa atgtggtatc gcttttacga tttaaatacc     1080
aatcgtggct tcttcagtga tcgcgatggc agcaaattct atgacatcac ccagatgtca     1140
gaagagcgct gcactggata tagctggggg ggtgattacg gcacgtcgat tatttccttc     1200
gcgcaaaaag tgggatattc gtaa                                     1224

```

```

<210> 62
<211> 407
<212> PRT
<213> Unknown

```

```

<220>
<223> Obtained from an environmental sample

```

```

<221> DOMAIN
<222> (0)...(407)
<223> Catalytic domain

```

```

<400> 62
Met Glu Leu Pro Val Thr Gly Ala Trp Ala Thr Trp Gln Thr Ala Thr
 1          5          10          15
Val Glu Ile Asp Leu Val Gln Gly Asn Leu Leu Lys Leu Ser Ala
 20          25          30
Ile Thr Ala Asp Gly Leu Ala Asn Ile Asp Ser Leu Lys Ile Asp Gly
 35          40          45
Ala Gln Thr Lys Ala Gly Val Cys Ser Thr Val Ala Ser Ser Ser Ser
 50          55          60
Ser Ser Val Ala Ser Ser Ile Lys Ser Ser Ser Ser Ser Ser Ser
 65          70          75          80
Ser Ser Thr Thr Thr Val Lys Thr Leu Thr Leu Asp Gly Asn Pro Ala
 85          90          95
Ala Asn Trp Phe Asn Lys Ser Arg Thr Lys Trp Asn Thr Ser Arg Ala
 100         105         110
Asp Val Val Leu Ser Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys Asn
 115         120         125
Leu Asp Tyr Asn Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser Gly
 130         135         140
Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu
 145         150         155         160
Val Tyr Lys Asn Gly Asn Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg
 165         170         175
Ala Ala Asn Phe Ile Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro

```

			180					185					190				
Gln	Phe	Tyr	Pro	Leu	Lys	Gly	Gly	Tyr	Ala	Asp	His	Ala	Thr	Phe	Asn		
		195					200					205					
Asp	Asn	Gly	Met	Ala	Tyr	Ala	Leu	Thr	Val	Leu	Asp	Phe	Ala	Val	Asn		
	210					215					220						
Lys	Arg	Ala	Pro	Phe	Asp	Thr	Asp	Val	Phe	Ser	Asp	Ser	Asp	Arg	Ala		
225					230					235					240		
Lys	Phe	Lys	Thr	Ala	Val	Ala	Lys	Gly	Val	Asp	Tyr	Ile	Leu	Lys	Ala		
				245					250					255			
Gln	Trp	Lys	Gln	Asn	Gly	Lys	Leu	Thr	Val	Trp	Cys	Ala	Gln	His	Gly		
		260					265						270				
Ala	Thr	Asp	Tyr	Gln	Pro	Lys	Lys	Ala	Arg	Ala	Tyr	Glu	Leu	Glu	Ser		
	275					280						285					
Leu	Ser	Gly	Ser	Glu	Ser	Val	Gly	Val	Leu	Ala	Phe	Leu	Met	Thr	Gln		
290					295						300						
Pro	Gln	Thr	Ala	Gln	Ile	Glu	Ala	Ala	Val	Lys	Ala	Gly	Val	Ala	Trp		
305				310					315						320		
Phe	Asn	Ser	Pro	Asn	Thr	Tyr	Leu	Asn	Asn	Tyr	Thr	Tyr	Asp	Ser	Ser		
				325				330						335			
Lys	Ala	Ser	Thr	Asn	Pro	Ile	Val	Ala	Lys	Ser	Gly	Ser	Lys	Met	Trp		
			340					345					350				
Tyr	Arg	Phe	Tyr	Asp	Leu	Asn	Thr	Asn	Arg	Gly	Phe	Phe	Ser	Asp	Arg		
	355					360					365						
Asp	Gly	Ser	Lys	Phe	Tyr	Asp	Ile	Thr	Gln	Met	Ser	Glu	Glu	Arg	Arg		
370					375					380							
Thr	Gly	Tyr	Ser	Trp	Gly	Gly	Asp	Tyr	Gly	Thr	Ser	Ile	Ile	Ser	Phe		
385				390					395						400		
Ala	Gln	Lys	Val	Gly	Tyr	Leu											
				405													

<210> 63

<211> 1023

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 63

atgttaagtt	tcatacgcggt	atcagtgttt	cataaattact	gtacagggga	gactgcggtcc	60
acaaaaaatt	cagtggccga	aaagatgctt	cagtaccagt	tgtcaaattgg	cgcctggccc	120
aaacagtttg	tagacaaaag	tgctggtgat	tacagtcttc	cattaacgaa	agagctccta	180
cagcagatca	agaaaacaga	tattgatcat	gctacgctcg	acaacagtcg	gacaaccgga	240
gaaataactg	aattgatcaa	ggcttttaag	gacactaaaa	ataaggcata	tttgactgct	300
gcagaaaagg	ggattgcata	tattttatcg	gctcaatatg	agaatggcgg	atttccacaa	360
tactacccaa	ataaattata	ctatagagct	gagataacat	acaacgatga	tgcatgatc	420
aatgcattac	tagtgcttta	caaagtagcc	aataagcgag	aggggtttga	ggctatcaat	480
cccatatttg	tgtcaaaaagc	gcaaaaagca	gttgaaaagg	gtataacctg	tatcctaaaa	540
acacaggtca	tacaagacgg	aaaaaggagt	atttgggctg	cgcaatacga	tcagaacact	600
ttacaacctg	ctcaggcaag	aaagtgtgaa	ccagcttcat	tgagcacaag	tgaatctgtt	660
tccatcgttc	gctttctcat	gctacagcct	gcaaccactg	aaattaagca	agcgatcgaa	720
catgcaatac	aatggttcga	acagcatgat	attgaagggt	accgtttcga	ccgcatacaa	780
gatagggtga	ctggaaaata	tcaacggcag	cttgctcgctg	atcggacttc	cacgatttgg	840
gcgcgatttt	ataatctcga	agacaaccgt	ccattgtttg	gagatcgga	caatacaatc	900
aaatacaact	ttgaggaggt	ttcagaggag	cgtagaaatg	gctatgcttg	gttcggcaac	960
tggccggaaa	agctgatcca	aaaggactat	ccaaaatgga	aaaaacaata	caaaattcaa	1020
taa						1023

<210> 64

<211>	340
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

```
<221> SIGNAL
<222> (1) ... (16)
```

```
<221> DOMAIN
<222> (17)...(340)
<223> Catalytic domain
```

<400>	64														
Met	Leu	Ser	Phe	Ile	Ala	Val	Ser	Val	Phe	His	Asn	Tyr	Cys	Thr	Gly
1				5					10					15	
Gln	Thr	Ala	Ser	Thr	Lys	Asn	Ser	Val	Ala	Glu	Lys	Met	Leu	Gln	Tyr
			20					25					30		
Gln	Leu	Ser	Asn	Gly	Ala	Trp	Pro	Lys	Gln	Leu	Val	Asp	Lys	Ser	Val
		35					40					45			
Val	Asp	Tyr	Ser	Leu	Pro	Leu	Thr	Lys	Glu	Leu	Leu	Gln	Gln	Ile	Lys
	50					55					60				
Lys	Thr	Asp	Ile	Asp	His	Ala	Thr	Leu	Asp	Asn	Ser	Ala	Thr	Thr	Arg
65					70					75					80
Glu	Ile	Thr	Glu	Leu	Ile	Lys	Ala	Phe	Lys	Asp	Thr	Lys	Asn	Lys	Ala
				85					90					95	
Tyr	Leu	Thr	Ala	Ala	Glu	Lys	Gly	Ile	Ala	Tyr	Ile	Leu	Ser	Ala	Gln
			100					105					110		
Tyr	Glu	Asn	Gly	Gly	Phe	Pro	Gln	Tyr	Tyr	Pro	Asn	Lys	Leu	Tyr	Tyr
		115					120					125			
Arg	Ala	Glu	Ile	Thr	Tyr	Asn	Asp	Asp	Ala	Met	Ile	Asn	Ala	Leu	Leu
	130					135					140				
Val	Leu	Tyr	Lys	Val	Ala	Asn	Lys	Arg	Glu	Gly	Phe	Glu	Ala	Ile	Asn
145					150					155					160
Pro	Ile	Phe	Val	Ser	Lys	Ala	Gln	Lys	Ala	Val	Glu	Lys	Gly	Ile	Thr
				165					170					175	
Cys	Ile	Leu	Lys	Thr	Gln	Val	Ile	Gln	Asp	Gly	Lys	Arg	Ser	Ile	Trp
			180					185					190		
Ala	Ala	Gln	Tyr	Asp	Gln	Asn	Thr	Leu	Gln	Pro	Ala	Gln	Ala	Arg	Lys
		195					200					205			
Phe	Glu	Pro	Ala	Ser	Leu	Ser	Thr	Ser	Glu	Ser	Val	Ser	Ile	Val	Arg
	210					215					220				
Phe	Leu	Met	Leu	Gln	Pro	Ala	Thr	Thr	Glu	Ile	Lys	Gln	Ala	Ile	Glu
225					230					235					240
His	Ala	Ile	Gln	Trp	Phe	Glu	Gln	His	Asp	Ile	Glu	Gly	Tyr	Arg	Phe
				245					250					255	
Asp	Arg	Ile	Gln	Asp	Arg	Val	Thr	Gly	Lys	Tyr	Gln	Arg	Gln	Leu	Val
			260					265					270		
Ala	Asp	Arg	Thr	Ser	Thr	Ile	Trp	Ala	Arg	Phe	Tyr	Asn	Leu	Glu	Asp
		275					280					285			
Asn	Arg	Pro	Leu	Phe	Gly	Asp	Arg	Asp	Asn	Thr	Ile	Lys	Tyr	Asn	Phe
	290					295					300				
Glu	Glu	Val	Ser	Glu	Glu	Arg	Arg	Asn	Gly	Tyr	Ala	Trp	Phe	Gly	Asn
305					310					315					320
Trp	Pro	Glu	Lys	Leu	Ile	Gln	Lys	Asp	Tyr	Pro	Lys	Trp	Lys	Lys	Gln
				325					330						

<210> 65
 <211> 1311
 <212> DNA
 <213> Bacteria

<400> 65
 gtgaaccgac gtacccgcct gggagcggtc gccgcgaccg ccctcgccct gacggtcacc 60
 gccccgcgcg ccggtgcca cgccgcgcgt cccacgcgcg cgccacgccc ggtcgccgat 120
 ccggctcgcg ccacgctgcc cgccggcgac ggctggggtt ccgaggggac cggcacgacc 180
 ggtgggggcg ccgcccagggc ctcccgggtc ttaccgctcg ccacctggga ggagttccgg 240
 gccgcgctcg ccggtgcccg ctccgagccc aggatcgta aggtgggtgg cacgctgaac 300
 gccaccgccc ccggtcgcg cgcccttcgag gcgcggggct acgacttcgc ccgctacctc 360
 gccgactacg acccgccggt gtgggggtac gagaaggagg tcagcgggcc gcaggaggag 420
 ctgccccgcg cgtccgcgac cgcgacgggc caggccatca aggtcaaggt gccggcgaac 480
 accacgatcg tcggggtcgg caggcacgcg gggatcacgg gcggcagcct ccaggtgcag 540
 ggcgtcgaca acgtcggtgt ccgcaacctg acgctggaga gccgctcga ctgcttccc 600
 cagtgggacc cgaccgacgg cgcgaccggg gcgtggaact ccgagtaga cagcctcgtc 660
 gtgtacggct ccacccatgt ctggatcgac cacaacacct tcaccgacgg cgcccaccg 720
 gacagttcgc tgcctcgtc ctacggcgag gtctaccagc agcacgacgg cgaactggac 780
 gtcgtgcggg gcgcggacct cgtcacggtc tcgtggaacg ccttcaccga ccacgacaag 840
 accctgatga tcggcaacag cgacagcgcg ggcgccaccg accggggcaa gctgcgggtc 900
 accctgcacc acaacctgtt cgagaacgtc gtcgagcggg cgccccgggt caggttcggg 960
 caggtcgacg cgtacaacaa ccacttcgtc gtgccgagtt cggcctacgc gtacagcctg 1020
 ggcgtcgggc aggagtcca gctcttcgcg gagaagaacg cgttcaccct cgccgggggc 1080
 gtgccggccg ggaagatcct caagaagtgg aaggacgcgc ccgtcaccac cgtcggcaac 1140
 tacgtgaacg gcaggccggt cgacctgtc gccgtccaca acaccagtt cccggaggag 1200
 cagttgcggg ccgacgcggg ctggaccccc gtcctgcgca ccagggtcga ccaccgagg 1260
 gccgtccccg cgctcgtcga ccaccgcgcg ggcgcgggcc gtcctgctg a 1311

<210> 66
 <211> 436
 <212> PRT
 <213> Bacteria

<220>

<221> SIGNAL
 <222> (1)...(28)

<221> DOMAIN
 <222> (29)...(436)
 <223> Catalytic domain

<400> 66
 Met Asn Arg Arg Thr Arg Leu Gly Ala Val Ala Ala Thr Ala Leu Ala
 1 5 10 15
 Leu Thr Val Thr Ala Pro Ala Ala Gly Ala His Ala Ala Ala Pro His
 20 25 30
 Ala Ala Pro Arg Pro Val Ala Asp Pro Ala Arg Ala Thr Leu Pro Ala
 35 40 45
 Gly Asp Gly Trp Ala Ser Glu Gly Thr Gly Thr Thr Gly Gly Ala Ala
 50 55 60
 Ala Glu Ala Ser Arg Val Phe Thr Val Ala Thr Trp Glu Glu Phe Arg
 65 70 75 80
 Ala Ala Leu Ala Val Pro Gly Ser Glu Pro Arg Ile Val Lys Val Val
 85 90 95
 Gly Thr Leu Asn Ala Thr Ala Ala Gly Cys Gly Ala Phe Glu Ala Pro
 100 105 110

Gly Tyr Asp Phe Ala Arg Tyr Leu Ala Asp Tyr Asp Pro Ala Val Trp
115 120 125
Gly Tyr Glu Lys Glu Val Ser Gly Pro Gln Glu Glu Leu Arg Ala Ala
130 135 140
Ser Ala Thr Ala Gln Gly Gln Ala Ile Lys Val Lys Val Pro Ala Asn
145 150 155 160
Thr Thr Ile Val Gly Val Gly Arg His Ala Gly Ile Thr Gly Gly Ser
165 170 175
Leu Gln Val Gln Gly Val Asp Asn Val Val Val Arg Asn Leu Thr Leu
180 185 190
Glu Ser Pro Leu Asp Cys Phe Pro Gln Trp Asp Pro Thr Asp Gly Ala
195 200 205
Thr Gly Ala Trp Asn Ser Glu Tyr Asp Ser Leu Val Val Tyr Gly Ser
210 215 220
Thr His Val Trp Ile Asp His Asn Thr Phe Thr Asp Gly Ala His Pro
225 230 235 240
Asp Ser Ser Leu Pro Ser Tyr Tyr Gly Glu Val Tyr Gln Gln His Asp
245 250 255
Gly Glu Leu Asp Val Val Arg Gly Ala Asp Leu Val Thr Val Ser Trp
260 265 270
Asn Ala Phe Thr Asp His Asp Lys Thr Leu Met Ile Gly Asn Ser Asp
275 280 285
Ser Ala Gly Ala Thr Asp Arg Gly Lys Leu Arg Val Thr Leu His His
290 295 300
Asn Leu Phe Glu Asn Val Val Glu Arg Ala Pro Arg Val Arg Phe Gly
305 310 315 320
Gln Val Asp Ala Tyr Asn Asn His Phe Val Val Pro Ser Ser Ala Tyr
325 330 335
Ala Tyr Ser Leu Gly Val Gly Gln Glu Ser Gln Leu Phe Ala Glu Lys
340 345 350
Asn Ala Phe Thr Leu Ala Gly Gly Val Pro Ala Gly Lys Ile Leu Lys
355 360 365
Lys Trp Lys Asp Ala Pro Val Thr Thr Val Gly Asn Tyr Val Asn Gly
370 375 380
Arg Pro Val Asp Leu Leu Ala Val His Asn Thr Gln Phe Pro Glu Glu
385 390 395 400
Gln Leu Arg Ala Asp Ala Gly Trp Thr Pro Val Leu Arg Thr Arg Val
405 410 415
Asp His Pro Arg Ala Val Pro Ala Leu Val Asp His Arg Ala Gly Ala
420 425 430
Gly Arg Ser Cys
435

<210> 67

<211> 1995

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 67

atgaaaaatt	caaaaactgt	ttttactgca	caaaaaaac	tcatgcactc	ttgcattgcc	60
gccgctatcg	gcttggcgat	aagttcaggt	gcttggtcag	cttgtactta	cactgtcacc	120
aataattggg	gttctggctt	caccggtgaa	atcaaagtta	ccaacaacac	atcatcggct	180
gtaaatgggt	ggctctgtgc	ttggcaggaa	tcaggcgcat	cagtcaccaa	ctcatggaac	240
gcaactctga	goggatcaaa	tccttatacg	gcagccgcct	taggttggaa	tgcaactctc	300
gcacccggtg	cttctgccag	ttttggcttt	caagcaaattg	gcactgctag	cgcacctaaa	360
gtgaatggca	ctttatgtgg	aacagctact	tcatcaaacac	ctgcgtcatc	cagcagtgtt	420

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gcgagttcgg ttaaatacaag cgcacccggt tcgtccagca gtaaatacat cagctcaatc 480
actgtgagta gtagttctat cgccagcagc agcgcaccaa gtgtttcttc attaacaatt 540
caggaagagc aagctgggtt ctgtcgtgtt gatggcattg caacagaaag caccaacacc 600
ggctttaccg gcaacggcta taccaatgca aacaacgcac aaggtgcagc gattgaatgg 660
gcggtaaatg caccgagcag tggccgctac acactcacat tccgttttgc aaatggcggc 720
actgcagcac gcaatgggtt actgttaatt aacggcggta gcaatggtaa ctacaccgtg 780
gattttaccac taaccggcgc atgggcgact tggcaaacag cgactgtaga aatcgatttg 840
gtacaaggca ccaacacgct gaaactttct gcattaaccg cagatggctt agctaataatc 900
gattcattaa aaattgatgg caaccaaccg aaagcaggca cttgcagcaa tacatcaagc 960
agtgttgcaa gcagttcttc atccgttaaa tccagttcaa gttcttcac aagctcatcc 1020
accactgcaa aaatgctgac tcttgatggc aaccccgccg caagttggtt caacaaatcc 1080
agaaccaaat ggaatagcag tcgtgcggac attgtgttgt cttaccagca agctaaccggc 1140
ggctggccaa aaaatctgga ttacaactca gtaagcgcag gtaatgggtg tagcgacagc 1200
ggcactatcg acaacggcgc aaccatcacg gaaatgggtt atctcgaga agtttataaa 1260
aacgggggca atacaaaata tcgcgatgca gtacgtaaag cggcaaaactt tattgtgagt 1320
tcgcaatata gcaactgggc gttaccacaa ttttaccat tgaaagggtg ttatgcagat 1380
cacgccacct ttaacgataa cggcatggct tacgcattaa cggtattgga ttttgcggtg 1440
aacaaacgtg cgccgtttga taacgatgta ttttctgat cagaccgcgc aaaattcaaa 1500
actgccgtga ccaaaggat tgattacatt ttgaaagccc aatggaaaaca aaatggaaaa 1560
ctcaccgcac ggtgtgcgca acacggagca aacgactatc aacaaaaagc ggcgcggtgt 1620
tatgagttag tatctttaag cggcagcgaa tccgttggca tcatcgcttt cctgatgacc 1680
caaccacaaa ctgcgcaaat cgaagcagcg gttaaagccg gtgtaaaactg gttcgctagc 1740
ccgaatacat acttggttaa ttacacctac gactcgtcaa aagcctctac caatccgatt 1800
gtgtacaaat ccggcagcag aatgtggtat cgcttctacg atctgaacac caatcgcgga 1860
ttcttttagtg atcgcgatgg cagcaaatc tatgacatca ctcaaatgtc tgaagaacgt 1920
cgcaccggct acagctgggg cggttcttac ggtgaatcga ttatcagctt cgcgcaaaaa 1980
gtgggttatc tctaa

```

<210> 68
 <211> 664
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(32)

<221> BINDING
 <222> (33)...(126)
 <223> Carbohydrate binding module

<221> BINDING
 <222> (184)...(307)
 <223> Carbohydrate binding module

<221> DOMAIN
 <222> (308)...(664)
 <223> Catalytic domain

<400> 68
 Met Lys Asn Ser Lys Thr Val Phe Thr Ala Gln Lys Lys Leu Met His
 1 5 10 15
 Ser Cys Ile Ala Ala Ile Gly Leu Ala Ile Ser Ser Gly Ala Trp
 20 25 30
 Ser Ala Cys Thr Tyr Thr Val Thr Asn Asn Trp Gly Ser Gly Phe Thr
 35 40 45
 Gly Glu Ile Lys Val Thr Asn Asn Thr Ser Ser Ala Val Asn Gly Trp

50	55	60
Ser Val Ser Trp Gln Glu Ser Gly Ala Ser Val Thr Asn Ser Trp Asn		
65	70	75
Ala Thr Leu Ser Gly Ser Asn Pro Tyr Thr Ala Ala Ala Leu Gly Trp		80
	85	90
Asn Ala Thr Leu Ala Pro Gly Ala Ser Ala Ser Phe Gly Phe Gln Ala		95
	100	105
Asn Gly Thr Ala Ser Ala Pro Lys Val Asn Gly Thr Leu Cys Gly Thr		110
	115	120
Ala Thr Ser Ser Thr Pro Ala Ser Ser Ser Ser Val Ala Ser Ser Val		125
	130	135
Lys Ser Ser Ala Pro Val Ser Ser Ser Ser Lys Ser Ser Ser Ser Ile		140
145	150	155
Thr Val Ser Ser Ser Ser Ile Ala Ser Ser Ser Ala Pro Ser Val Ser		160
	165	170
Ser Leu Thr Ile Gln Glu Glu Gln Ala Gly Phe Cys Arg Val Asp Gly		175
	180	185
Ile Ala Thr Glu Ser Thr Asn Thr Gly Phe Thr Gly Asn Gly Tyr Thr		190
	195	200
Asn Ala Asn Asn Ala Gln Gly Ala Ala Ile Glu Trp Ala Val Asn Ala		205
	210	215
Pro Ser Ser Gly Arg Tyr Thr Leu Thr Phe Arg Phe Ala Asn Gly Gly		220
225	230	235
Thr Ala Ala Arg Asn Gly Ser Leu Leu Ile Asn Gly Gly Ser Asn Gly		240
	245	250
Asn Tyr Thr Val Asp Leu Pro Leu Thr Gly Ala Trp Ala Thr Trp Gln		255
	260	265
Thr Ala Thr Val Glu Ile Asp Leu Val Gln Gly Thr Asn Thr Leu Lys		270
	275	280
Leu Ser Ala Leu Thr Ala Asp Gly Leu Ala Asn Ile Asp Ser Leu Lys		285
	290	295
Ile Asp Gly Asn Gln Pro Lys Ala Gly Thr Cys Ser Asn Thr Ser Ser		300
305	310	315
Ser Val Ala Ser Ser Ser Ser Val Lys Ser Ser Ser Ser Ser Ser		320
	325	330
Ser Ser Ser Ser Thr Thr Ala Lys Met Leu Thr Leu Asp Gly Asn Pro		335
	340	345
Ala Ala Ser Trp Phe Asn Lys Ser Arg Thr Lys Trp Asn Ser Ser Arg		350
	355	360
Ala Asp Ile Val Leu Ser Tyr Gln Gln Ala Asn Gly Gly Trp Pro Lys		365
	370	375
Asn Leu Asp Tyr Asn Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser		380
385	390	395
Gly Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala		400
	405	410
Glu Val Tyr Lys Asn Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg		415
	420	425
Lys Ala Ala Asn Phe Ile Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu		430
	435	440
Pro Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe		445
	450	455
Asn Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val		460
465	470	475
Asn Lys Arg Ala Pro Phe Asp Asn Asp Val Phe Ser Asp Ala Asp Arg		480
	485	490
Ala Lys Phe Lys Thr Ala Val Thr Lys Gly Ile Asp Tyr Ile Leu Lys		495
	500	505
Ala Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His		510
	515	520
		525

Gly Ala Asn Asp Tyr Gln Pro Lys Ala Ala Arg Ala Tyr Glu Leu Val
 530 535 540
 Ser Leu Ser Ser Gly Ser Glu Ser Val Gly Ile Ile Ala Phe Leu Met Thr
 545 550 555 560
 Gln Pro Gln Thr Ala Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn
 565 570 575
 Trp Phe Ala Ser Pro Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser
 580 585 590
 Ser Lys Ala Ser Thr Asn Pro Ile Val Tyr Lys Ser Gly Ser Arg Met
 595 600 605
 Trp Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp
 610 615 620
 Arg Asp Gly Ser Lys Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg
 625 630 635 640
 Arg Thr Gly Tyr Ser Trp Gly Gly Ser Tyr Gly Glu Ser Ile Ile Ser
 645 650 655
 Phe Ala Gln Lys Val Gly Tyr Leu
 660

<210> 69
 <211> 1035
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 69
 atggcgcggtt tgttccggtg cgtgtgtgcc agcctgggag gatgggcccgc ggttctggcc 60
 gccgcggcgg gcccggtattg gtccgcctg ctgcgcgaac cggacccttg gtttcgcagt 120
 ccggcggggc aacaggcgggt gacgaacgtt ttgtcctggc agagcgcgac aggcgccttg 180
 ccgaaaaacc tggacaccac ccgcgagccg cgtcggcagg attccgcccc gcccgagggc 240
 accttcgaca acggcgccac caccggcgag ttgcggtttc tggcgcgggc gtttgcggcc 300
 accggcgatc cgcgctgcga agccgcgggtg ctccgggggc tggacggcat cctcgcggcc 360
 cagcttccca gcggcggtg gccgcagtgt catcctccgc gcgcgcctta tcagcgccac 420
 atcaccttca acgacgggtg catggtgcgc atcctggagc tgctgcgcga gatagaccgc 480
 gcgcgggagt ttcgctgggt ggacgaggcg cggcgcgcgc gggcgcgcgc ggccttcaact 540
 cgcgggctgg agtgccctct gcgctgccag gtggtcgtcg agggcagact caccgtgtgg 600
 tgtgcccagc atgacgcgga gaactttcaa ccgcgaccgg cacgcgccta cgaactggaa 660
 tcgctcagcg gcgcggaaaag cgcggcgcgc ctggtgttcc tcatgagcct ggagccgcca 720
 acccgcgaga tcgcgcgcgc ggctcgaggcc gggcgggcct ggttttcggc ggtaaagctt 780
 gaagggttcc gtctcgaacg aacggccgac gacgcgcggg tgggtggaaga gccgggcgcg 840
 ccgcgcgtct gggcgcggtt ctacgagatc gggaccaatc gccccatctt tgccggtcgc 900
 gacggtgtca agaagtacgc cctgagcgag atcgagcggg aacgccgggt cggctatgcg 960
 tggtagcggc cctgggggtga accggtcgcc cgccattatg cccagtggcg ggagcgttac 1020
 gggacgcaga aatga 1035

<210> 70
 <211> 344
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(22)

<221> DOMAIN

<222> (23)...(344)

<223> Catalytic domain

<400> 70

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Met Ala Arg Leu Phe Arg Cys Val Cys Ala Ser Leu Gly Gly Trp Ala
 1           5           10           15
Ala Val Leu Ala Ala Ala Ala Gly Pro Asp Trp Ser Arg Leu Leu Ala
      20           25           30
Gln Pro Asp Pro Trp Phe Arg Ser Pro Ala Gly Gln Gln Ala Val Thr
      35           40           45
Asn Val Leu Ser Trp Gln Ser Ala Thr Gly Ala Trp Pro Lys Asn Leu
      50           55           60
Asp Thr Thr Arg Glu Pro Arg Arg Gln Asp Ser Ala Pro Pro Glu Gly
      65           70           75           80
Thr Phe Asp Asn Gly Ala Thr Thr Gly Glu Leu Arg Phe Leu Ala Arg
      85           90           95
Ala Phe Ala Ala Thr Gly Asp Pro Arg Cys Glu Ala Ala Val Leu Arg
      100          105          110
Gly Leu Asp Gly Ile Leu Ala Ala Gln Leu Pro Ser Gly Gly Trp Pro
      115          120          125
Gln Cys His Pro Pro Arg Ala Pro Tyr Gln Arg His Ile Thr Phe Asn
      130          135          140
Asp Gly Val Met Val Arg Ile Leu Glu Leu Leu Arg Glu Ile Asp Arg
      145          150          155          160
Ala Pro Glu Phe Arg Trp Val Asp Glu Ala Arg Arg Ala Arg Val Arg
      165          170          175
Ala Ala Phe Thr Arg Gly Leu Glu Cys Leu Leu Arg Cys Gln Val Val
      180          185          190
Val Glu Gly Arg Leu Thr Val Trp Cys Ala Gln His Asp Ala Glu Asn
      195          200          205
Phe Gln Pro Arg Pro Ala Arg Ala Tyr Glu Leu Glu Ser Leu Ser Gly
      210          215          220
Ala Glu Ser Ala Gly Ile Leu Val Phe Leu Met Ser Leu Glu Pro Pro
      225          230          235          240
Thr Pro Glu Ile Ala Arg Ala Val Glu Ala Gly Ala Ala Trp Phe Ser
      245          250          255
Ala Val Lys Leu Glu Gly Phe Arg Leu Glu Arg Thr Ala Asp Asp Ala
      260          265          270
Arg Val Val Glu Glu Pro Gly Ala Pro Pro Leu Trp Ala Arg Phe Tyr
      275          280          285
Glu Ile Gly Thr Asn Arg Pro Ile Phe Ala Gly Arg Asp Gly Val Lys
      290          295          300
Lys Tyr Ala Leu Ser Glu Ile Glu Arg Glu Arg Arg Val Gly Tyr Ala
      305          310          315          320
Trp Tyr Gly Ala Trp Gly Glu Pro Val Ala Arg His Tyr Ala Gln Trp
      325          330          335
Arg Glu Arg Tyr Gly Thr Gln Lys
      340

```

<210> 71

<211> 1038

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 71

gtgactcgtg tcgcccttgc gatggggctt gttgcatggg ttccggcgct cgcttcagct

60

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gggcccgcgtg catatttgca gaagccggac gactgggttcg ccagtcccga ggccagggca 120
atcgccgcga acgtactcgc gcatcaggcc gatctcggcg ggtggccgaa gaacatcgac 180
acaaccgaagc cggttcaccgg cgaccggacg caaatcaaac cgaccttcga taacagcgcg 240
acaaccgacg agctccggtt tctggcgcg atccacaacg cgactcgcg cgagaagtac 300
cgcaccgcgt tcgagaagg gctcgattac atcttgaaag cacaatacgc aaacggcggt 360
tggcgcgagt cgcacccgcc cggcaccggc taccaccggc acatcacctt caacgacaat 420
gccatggtcc gtttgatgga gctcgtgcgc gaagtgcgca cctcgaatcg gtacgacttc 480
ctggacgccg accgccgcaa ggcctgccgc gccgctttcg atcgcggcgt cgaatgcac 540
ctgaagtgcc agatcaaggt cgacagtaag ctgacggcat ggtgcgccc gcacgacgag 600
aaggacctcg ctccccggcc ggcgcggacc tacgagctcg tctcactcag cggctcggag 660
tcggtcggga tcgtccgcct actcatgagc ctcgatcgac caagcccgga ggtcgtcgg 720
gccatcgacg gcgcggtcgc gtggttccag tcggcgaagc tcgaaggcac caaggtcgtt 780
gtcgagcgcg acccgaagta tccggcgcc cgggaacgcg tgggtggtgaa ggatccaaag 840
gcaccgccac tctggcgcg cttctacgaa atcggcacga atcgcccat cttctccgac 900
cgcgacggca tcaagaagta cgcgctcgcc gagatcggcc ccgaacggcg gaatggctat 960
gcctggtatg gcacctggcc gcgcgacctg ctggagaagg aatacccagg gtggaaaaag 1020
aagctggccc ggccgtga 1038

```

<210> 72
 <211> 345
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(20)

<221> DOMAIN
 <222> (21)...(345)
 <223> Catalytic domain

<400> 72

Met	Thr	Arg	Val	Ala	Leu	Ala	Met	Gly	Leu	Val	Ala	Trp	Val	Pro	Ala
1				5				10						15	
Leu	Ala	Ser	Ala	Gly	Pro	Ala	Ala	Tyr	Leu	Gln	Lys	Pro	Asp	Asp	Trp
			20					25					30		
Phe	Ala	Ser	Pro	Glu	Ala	Arg	Ala	Ile	Ala	Ala	Asn	Val	Leu	Ala	His
		35					40					45			
Gln	Ala	Asp	Leu	Gly	Gly	Trp	Pro	Lys	Asn	Ile	Asp	Thr	Thr	Lys	Pro
	50				55						60				
Phe	Thr	Gly	Asp	Arg	Thr	Gln	Ile	Lys	Pro	Thr	Phe	Asp	Asn	Ser	Ala
65					70					75				80	
Thr	Thr	Asp	Glu	Leu	Arg	Phe	Leu	Ala	Arg	Ile	His	Asn	Ala	Thr	Arg
				85					90					95	
Asp	Glu	Lys	Tyr	Arg	Thr	Ala	Phe	Glu	Lys	Gly	Leu	Asp	Tyr	Ile	Leu
			100					105					110		
Lys	Ala	Gln	Tyr	Ala	Asn	Gly	Gly	Trp	Pro	Gln	Ser	His	Pro	Pro	Gly
		115					120					125			
Thr	Gly	Tyr	His	Arg	His	Ile	Thr	Phe	Asn	Asp	Asn	Ala	Met	Val	Arg
	130					135					140				
Leu	Met	Glu	Leu	Val	Arg	Glu	Val	Ala	Thr	Ser	Asn	Arg	Tyr	Asp	Phe
145					150					155				160	
Leu	Asp	Ala	Asp	Arg	Arg	Lys	Ala	Cys	Arg	Ala	Ala	Phe	Asp	Arg	Gly
				165					170					175	
Ile	Glu	Cys	Ile	Leu	Lys	Cys	Gln	Ile	Lys	Val	Asp	Ser	Lys	Leu	Thr
		180					185						190		
Ala	Trp	Cys	Ala	Gln	His	Asp	Glu	Lys	Asp	Leu	Ala	Pro	Arg	Pro	Ala

```

      195              200              205
Arg Thr Tyr Glu Leu Val Ser Leu Ser Gly Ser Glu Ser Val Gly Ile
      210              215              220
Val Arg Leu Leu Met Ser Leu Asp Arg Pro Ser Pro Glu Val Ala Arg
      225              230              235              240
Ala Ile Asp Gly Ala Val Ala Trp Phe Gln Ser Ala Lys Leu Glu Gly
      245              250              255
Thr Lys Val Val Val Glu Arg Asp Pro Lys Tyr Pro Gly Gly Arg Glu
      260              265              270
Arg Val Val Val Lys Asp Pro Lys Ala Pro Pro Leu Trp Ala Arg Phe
      275              280              285
Tyr Glu Ile Gly Thr Asn Arg Pro Ile Phe Ser Asp Arg Asp Gly Ile
      290              295              300
Lys Lys Tyr Ala Leu Ala Glu Ile Gly Pro Glu Arg Arg Asn Gly Tyr
      305              310              315              320
Ala Trp Tyr Gly Thr Trp Pro Arg Asp Leu Leu Glu Lys Glu Tyr Pro
      325              330              335
Gly Trp Lys Lys Lys Leu Ala Arg Pro
      340              345

```

<210> 73
 <211> 1221
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

```

<400> 73
atgctcacca aaacatcact acttattgca ttgctaggca gttgttgtat cgcaccatta      60
catgcgagaca caccagcaag caatgcaccg acaaccaatg catcaattcc gctacagcaa      120
actgcgagcgc atgctgccgc ctggaaaaat tatctcgcca aatccaacga gttgcgcaaa      180
gcagaccagg cgagctcaa agccgagctg aaaaaactcg ggcaaaaaac cgcgagtttg      240
cctgagtaca ccaaagaatt tggttttgaa gtgaagcagt catctgagtg gtttaaaagc      300
actgaaggta aacgagtgat ggatattatc ctatcgtttc aaactccttc tggcggctgg      360
tcaaaaacgca ctgacatgag caaagcgccg cgcaaacccg gccaggcatt tgggtgtgaa      420
aaaaattaca tccccacctt tgataatggc gcgaccagca cacaattaat gctactggca      480
caggcgcatc aagccactgg cgataaacgc tacagcgatg catttgcgcg cgggcttgaa      540
tttatcatca ccgctcaata tccaatggc ggctggccac aaaattttcc attggttggc      600
aagtatcacg atcacatcac ttacaacgat gccctgatgc gcgatttaat ggtagtgcta      660
cacaagggtg ccatggccaa ggatgaattt gcctttgtat ccaaggcgca gcaacaggcc      720
gcacaagcga gcctcgaacg cgcgctggac tgcgttttga aaaccaggt gatggccaat      780
ggccaattaa ctatatgggg tgcgcagcac gatgccaaaa ccttaaaacc cgccaaagcg      840
cgcgccctatg aaatgatttc actcaccagt tctgaaagcg tgtggatgct cgatttttta      900
atggatttgc aacagcccag cgctgacatt attaaatccg tgcacgcggc tgccgcttgg      960
tatgagcaaa ataaaattat cggaaaaacc tggaccgggg gcgacacagt tctgaaagac      1020
gataaggatg caccgccaat ctgggcgcgt ttttatgaga taggtacgaa caaaccctg      1080
tttggcgacc gcgatgactc tgtccattac gatctggcaa aggtatcgga agagcgccgc      1140
acgggttatg cctggtacac aacctcacc aatcagggtat taaaaaagta cgcgcgctgg      1200
gctaaacaat atccgcaata a                                1221

```

<210> 74
 <211> 406
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(22)

<221> DOMAIN
 <222> (23)...(406)
 <223> Catalytic domain

<400> 74

Met	Leu	Thr	Lys	Thr	Ser	Leu	Leu	Ile	Ala	Leu	Leu	Gly	Ser	Cys	Cys
1				5					10					15	
Ile	Ala	Pro	Leu	His	Ala	Asp	Thr	Pro	Ala	Ser	Asn	Ala	Pro	Thr	Thr
			20					25					30		
Asn	Ala	Ser	Ile	Pro	Leu	Gln	Gln	Thr	Ala	Ser	Asp	Ala	Ala	Ala	Trp
		35				40						45			
Lys	Asn	Tyr	Leu	Ala	Lys	Ser	Asn	Glu	Leu	Arg	Lys	Ala	Asp	Gln	Ala
	50					55					60				
Gln	Leu	Lys	Ala	Glu	Leu	Lys	Lys	Leu	Gly	Gln	Lys	Thr	Ala	Ser	Leu
65					70					75					80
Pro	Glu	Tyr	Thr	Lys	Glu	Phe	Gly	Phe	Glu	Val	Lys	Gln	Ser	Ser	Glu
				85					90					95	
Trp	Phe	Lys	Ser	Thr	Glu	Gly	Lys	Arg	Val	Met	Asp	Ile	Ile	Leu	Ser
				100				105					110		
Phe	Gln	Thr	Pro	Ser	Gly	Gly	Trp	Ser	Lys	Arg	Thr	Asp	Met	Ser	Lys
		115				120						125			
Ala	Pro	Arg	Lys	Pro	Gly	Gln	Ala	Phe	Gly	Val	Glu	Lys	Asn	Tyr	Ile
		130				135					140				
Pro	Thr	Phe	Asp	Asn	Gly	Ala	Thr	Ser	Thr	Gln	Leu	Met	Leu	Leu	Ala
145					150					155					160
Gln	Ala	His	Gln	Ala	Thr	Gly	Asp	Lys	Arg	Tyr	Ser	Asp	Ala	Phe	Ala
				165					170					175	
Arg	Gly	Leu	Glu	Phe	Ile	Ile	Thr	Ala	Gln	Tyr	Pro	Asn	Gly	Gly	Trp
			180					185					190		
Pro	Gln	Asn	Phe	Pro	Leu	Val	Gly	Lys	Tyr	His	Asp	His	Ile	Thr	Tyr
		195					200					205			
Asn	Asp	Ala	Leu	Met	Arg	Asp	Leu	Met	Val	Val	Leu	His	Lys	Val	Ala
		210				215					220				
Met	Ala	Lys	Asp	Glu	Phe	Ala	Phe	Val	Ser	Lys	Ala	Gln	Gln	Gln	Ala
225					230					235					240
Ala	Gln	Ala	Ser	Leu	Glu	Arg	Ala	Leu	Asp	Cys	Val	Leu	Lys	Thr	Gln
				245					250					255	
Val	Met	Ala	Asn	Gly	Gln	Leu	Thr	Ile	Trp	Gly	Ala	Gln	His	Asp	Ala
			260					265					270		
Lys	Thr	Leu	Lys	Pro	Ala	Lys	Ala	Arg	Ala	Tyr	Glu	Met	Ile	Ser	Leu
			275				280					285			
Thr	Ser	Ser	Glu	Ser	Val	Trp	Met	Leu	Asp	Phe	Leu	Met	Asp	Leu	Gln
		290				295					300				
Gln	Pro	Ser	Ala	Asp	Ile	Ile	Lys	Ser	Val	His	Ala	Ala	Ala	Ala	Trp
305					310					315					320
Tyr	Glu	Gln	Asn	Lys	Ile	Ile	Gly	Lys	Thr	Trp	Thr	Arg	Gly	Asp	Thr
				325					330					335	
Val	Leu	Lys	Asp	Asp	Lys	Asp	Ala	Pro	Pro	Ile	Trp	Ala	Arg	Phe	Tyr
			340				345						350		
Glu	Ile	Gly	Thr	Asn	Lys	Pro	Leu	Phe	Gly	Asp	Arg	Asp	Asp	Ser	Val
		355					360					365			
His	Tyr	Asp	Leu	Ala	Lys	Val	Ser	Glu	Glu	Arg	Arg	Thr	Gly	Tyr	Ala
		370				375					380				
Trp	Tyr	Thr	Thr	Ser	Pro	Asn	Gln	Val	Leu	Lys	Lys	Tyr	Ala	Arg	Trp
385					390					395					400
Ala	Lys	Gln	Tyr	Pro	Gln										

405

<210> 75
 <211> 1767
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 75
 atgaccacaa cccgccgcac tatcctgaaa gccgccgccca gccgccggcgc gatcgccagc 60
 accggctggc ccgccttggc cgccgcacag gccgccgaag ccgccgaccc gtgggcccgc 120
 gccagcaga tcatcgaccg ctctgccaag ccgctcagct tcccgaaacag ggacttcccg 180
 atcaccgagt tcggcgccaa accctgcaag ctggtcaaag cccagggcct ggtcgaagta 240
 agagtcaaag gcgaactcga aacgccagca ccgcaagcgc cggacgccta cccggcaatc 300
 aaagccgccca tcgccgcagc gagcaaggcc ggaggagggc gcgtgctgat cccggccggc 360
 aactggtact gcaagggcc tatcgtgctg ctgtcgaacg tgcacgtgca ccttgccaag 420
 ggccgcgaag tctacttcag cgccaacgcc aaggacttcg cccgcgacgg cgactacgac 480
 tggcgcccca acggcaagct ggtgctctcg cgctggcaag gcaacgattg cctgaacttc 540
 tcgcccattg tctacgcgcg cgggcaaaaag aatatcgcca ttaccggcga agactggacc 600
 agcatcctga acggccaggc cggcgtggcg ttcgaagacg gcagcggcaa tggttggtg 660
 ggcatgaacc ccgccggcgc gccgcccgcc agcaccacgc accagggcgc agccaatccg 720
 aacaacgccg aggagccaat cgccagactg cccacgcgcc acgcgaactg gagcgccgac 780
 gacaagtacc tgccgtgct gtccgaagcc ggcggtgccg ccgagcgccg cgtgttcgg 840
 ctggggcact acctgcggcc gtcgatggtc gaattcgctg actgcgggga tgtgctgatg 900
 cagggtacc aggtcatcaa cacgccgttc tggattcatc acccggtcaa ctcacgcaac 960
 attcacttct ccaaagtgcg catggaaagc atcggcccga attcggacgg ttctgatccc 1020
 gagtcttcg acaccatcct ggtggacggc tgcctgttca ataccggcga cgactgcac 1080
 gccatcaaat ccggcaagaa ccgagactcg caatacggcc caacgcgcaa tatggtggtc 1140
 cagaactgca tcatgaaccg cggccacggc ggcgttacgc tgggcagcga aatggcgggt 1200
 ggcatcgagc atatctacgc gcagaaaatc gaattccgca acgcgttctg ggaccacgac 1260
 ccgctgggca cggccatccg aatgaagacg aacatgaacc gcggcggcta ccttcgtcat 1320
 ttctacgtgc gcgacgtgac gctgccgaat ggcggtgcgta ccaagagcgg cttctacaag 1380
 acgctgccgg gatctccgct ggcaaggcaag gtctccacca gcggcgggcgc tgttatcact 1440
 atcgactgcg attacgcgcc gaatgacgac agcgtgcgcg tgcggccgcc gcaggtgctg 1500
 gacgtgcata tctcgaacgt ccgcgtcagc aatgtgaaaa cggccgaagg ctggttctcc 1560
 tgctaccagg ccatggtgct gctcggggccc gtggcggccca gcttcaacgg cgcgcctggc 1620
 acggccatcc tgccgatcac gaatgtcacc gtcagcgatt cggacttcgg cagcgcgcgc 1680
 aacagcgag agccctggtt cgcgttcaac gtgcagggac tcaagctgcg caacgtgcgc 1740
 atcgatggca aggagtacaa cgtatga 1767

<210> 76
 <211> 588
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(34)

<221> DOMAIN
 <222> (110)...(555)
 <223> Catalytic domain

<400> 76
 Met Thr Thr Thr Arg Arg Thr Ile Leu Lys Ala Ala Ala Ser Ala Gly

1	5	10	15
Ala Ile Ala Ser Thr Gly Trp Pro Ala Leu Ala Ala Ala Gln Ala Ala			
	20	25	30
Gln Ala Ala Asp Pro Trp Ala Arg Ala Gln Gln Ile Ile Asp Arg Phe			
	35	40	45
Ala Lys Pro Leu Ser Phe Pro Asn Arg Asp Phe Pro Ile Thr Glu Phe			
	50	55	60
Gly Ala Lys Pro Cys Lys Leu Val Lys Ala Gln Gly Leu Val Glu Val			
65	70	75	80
Arg Val Lys Gly Glu Leu Glu Thr Pro Ala Pro Gln Ala Pro Asp Ala			
	85	90	95
Tyr Pro Ala Ile Lys Ala Ala Ile Ala Ala Ala Ser Lys Ala Gly Gly			
	100	105	110
Gly Arg Val Leu Ile Pro Ala Gly Asn Trp Tyr Cys Lys Gly Pro Ile			
	115	120	125
Val Leu Leu Ser Asn Val His Val His Leu Ala Lys Gly Ala Gln Val			
	130	135	140
Tyr Phe Ser Ala Asn Ala Lys Asp Phe Ala Arg Asp Gly Asp Tyr Asp			
145	150	155	160
Cys Gly Ala Asn Gly Lys Leu Val Leu Ser Arg Trp Gln Gly Asn Asp			
	165	170	175
Cys Leu Asn Phe Ser Pro Met Val Tyr Ala Arg Gly Gln Lys Asn Ile			
	180	185	190
Ala Ile Thr Gly Glu Asp Trp Thr Ser Ile Leu Asn Gly Gln Ala Gly			
	195	200	205
Val Ala Phe Glu Asp Gly Ser Gly Asn Gly Trp Trp Gly Met Asn Pro			
	210	215	220
Ala Gly Ala Pro Pro Gly Ser Thr Thr His Gln Gly Ala Ala Asn Pro			
225	230	235	240
Asn Asn Ala Glu Glu Pro Ile Ala Arg Leu Pro Thr Arg His Ala Asn			
	245	250	255
Trp Ser Ala Asp Asp Lys Tyr Leu Pro Leu Leu Ser Glu Ala Gly Val			
	260	265	270
Pro Ala Glu Arg Arg Val Phe Gly Leu Gly His Tyr Leu Arg Pro Ser			
	275	280	285
Met Val Glu Phe Val Asp Cys Gly Asp Val Leu Met Gln Gly Tyr Gln			
	290	295	300
Val Ile Asn Thr Pro Phe Trp Ile His His Pro Val Asn Ser Arg Asn			
305	310	315	320
Ile His Phe Ser Lys Val Arg Met Glu Ser Ile Gly Pro Asn Ser Asp			
	325	330	335
Gly Phe Asp Pro Glu Ser Cys Asp Thr Ile Leu Val Asp Gly Cys Leu			
	340	345	350
Phe Asn Thr Gly Asp Asp Cys Ile Ala Ile Lys Ser Gly Lys Asn Arg			
	355	360	365
Asp Ser Gln Tyr Gly Pro Thr Arg Asn Met Val Val Gln Asn Cys Ile			
	370	375	380
Met Asn Arg Gly His Gly Gly Val Thr Leu Gly Ser Glu Met Ala Gly			
385	390	395	400
Gly Ile Glu His Ile Tyr Ala Gln Lys Ile Glu Phe Arg Asn Ala Phe			
	405	410	415
Trp Asp His Asp Pro Leu Gly Thr Ala Ile Arg Met Lys Thr Asn Met			
	420	425	430
Asn Arg Gly Tyr Leu Arg His Phe Tyr Val Arg Asp Val Thr Leu			
	435	440	445
Pro Asn Gly Val Arg Thr Lys Ser Gly Phe Tyr Lys Thr Leu Pro Gly			
	450	455	460
Ser Pro Leu Ala Gly Lys Val Ser Thr Ser Gly Gly Ala Val Ile Thr			
465	470	475	480

Ile	Asp	Cys	Asp	Tyr 485	Ala	Pro	Asn	Asp	Asp 490	Ser	Val	Arg	Val	Arg 495	Pro
Pro	Gln	Val	Ser	Asp 500	Val	His	Ile	Ser	Asn 505	Val	Arg	Val	Ser	Asn 510	Val
Lys	Thr	Ala	Glu	Gly 515	Ser	Phe	Ser	Cys	Tyr 520	Gln	Ala	Met 525	Val	Leu	Leu
Gly	Pro	Val	Ala	Ala 530	Ser	Phe 535	Asn	Gly	Ala	Pro	Gly 540	Thr	Ala	Ile	Leu
Pro 545	Ile	Thr	Asn	Val 550	Thr	Val	Ser	Asp	Ser 555	Asp	Phe	Gly	Thr	Pro	Arg 560
Asn	Ser	Ala	Glu	Pro 565	Trp	Phe	Ala	Phe	Asn 570	Val	Gln	Gly	Leu	Lys 575	Leu
Arg	Asn	Val	Arg 580	Ile	Asp	Gly	Lys	Glu 585	Tyr	Asn	Val				

<210>	77
<211>	2043
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<400>	77						
atgaaaacct	ccagagcaat	tttactaca	tcaacacctt	tacaccgcgc	gcttatcgcg		60
gctagtgtca	gcatggcaat	gagttctgcc	gcatgggcgc	gttgtacct	taccgtcacc		120
aataattggg	gctcaggatt	taccggcgaa	atcaaagtga	ccaacaacac	caccgccagc		180
gtgaacaatt	ggtctgtgtc	atggcaggaa	tccggtgcgc	ctatcaccaa	cgcttggaat		240
gcaacgctca	gtggctcaaa	cccttacaca	gccgatctcg	ctgttgtaa	tggcacactt		300
gccccaatg	cattggccac	ttttggttc	caggcaaacg	gtttgcgcg	tgcacctaaa		360
gtgaatggca	gcttgtgcgg	caccaacact	tcatcaacac	cggcatccag	cagtgttgcc		420
agctcggtta	aatcaagcgc	gcccgtatcg	tccagcagca	gatcatccag	ttcaatcgct		480
atcactagca	gctcttttagc	gagaagttct	attgcctcca	gcagctcact	agttagtagc		540
tccagagcga	gcagtagtgc	gccaagcggt	ttctctttta	cgatccaggga	agagcaagcg		600
ggcttctgtc	gtgttgatgg	cattgcgaca	gaaagcacca	acaccggttt	taccggcaat		660
ggctacacca	atgcgaacaa	cgcgcgaagg	gcagcgattg	aatggcgagt	cagcgcacct		720
agcagtgccc	gttatatacgt	agccttcgc	ttcgccaatg	gcggcacagc	agcgcgcaac		780
ggctcgttgt	taatcaatgg	ggtagcaat	ggtaattaca	ctgtggagtt	accctgacc		840
ggcgcatggg	caacctggca	aattgccagc	gtggaaattg	atttagtgca	aggcaataat		900
attttaaaaac	tctcggcggt	aaccgctgac	ggtttggcca	atatcgactc	attaaaaata		960
gacggcgcg	aaaccaaaagc	aggtacttgc	agcactacat	caagcagcag	cgttgccagc		1020
agctcgtcgt	ccgttaaatac	cagcgcaagt	tcttcttcga	gttcattccac	cgctgcaaaa		1080
atactgacat	tagacggtaa	cccgcccgct	agctggttca	acaaatccag	gaccaagtgg		1140
aatagcacgc	gcgcgcatat	tgtgttgtct	taccagcaat	ccaagcgcg	ttggccaaaa		1200
aacctggatt	acaactcagt	gagcgcaggc	aatggcggga	gcgacagcgg	caccatcgac		1260
aatggtgcaa	ccattaccga	aatggtttac	ctcgctgaaa	tttataaaaa	cggcggcaac		1320
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acaggcgct	tgccacaatt	ttatcogttg	aaaggcggct	atgcggatca	tgcgaccttt		1440
aacgataacg	gcattggcgta	cgcgttgacg	gtattggatt	tcgcagtaaa	caaacgcgca		1500
ccgtttgata	acgacatttt	ctctgatttc	gatcgggcga	aattcaaaac	cgctgttgcc		1560
aaaggtgtgg	attacatttt	aaaagccag	tggaaacaaa	attggaaaact	cactgctagg		1620
tgtgcacacg	acggtgctac	ggattaccaa	ccgaaaaaag	cgcgcgctta	tgaattggaa		1680
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gcgcaaatcg	aagcggcggt	caaggcgggt	gtcaactggt	tcgccagtcc	aaatacttat		1800
ttggctaact	acacttacga	ttcatcaaaa	gcgtctacca	acccgattgt	gtataaatcc		1860
ggaagcagaa	tgtggtatcg	cttctatgac	ctgaacacca	accgtggttt	ctttagtgat		1920
cgcgatggca	gcaaatctta	tgatatcacc	caaatgtcag	aagagcgtcg	caccggttat		1980
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taa							2043

<210> 78
 <211> 680
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(33)

<221> BINDING
 <222> (34)...(126)
 <223> Carbohydrate binding module

<221> BINDING
 <222> (199)...(322)
 <223> Carbohydrate binding module

<221> DOMAIN
 <222> (323)...(680)
 <223> Catalytic domain

<400> 78
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 Ala Leu Ile Ala Ala Ser Val Ser Met Ala Met Ser Ser Ala Ala Trp
 20 25 30
 Ala Gly Cys Thr Tyr Thr Val Thr Asn Asn Trp Gly Ser Gly Phe Thr
 35 40 45
 Gly Glu Ile Lys Val Thr Asn Thr Thr Ala Ser Val Asn Asn Trp
 50 55 60
 Ser Val Ser Trp Gln Glu Ser Gly Ala Ala Ile Thr Asn Ala Trp Asn
 65 70 75 80
 Ala Thr Leu Ser Gly Ser Asn Pro Tyr Thr Ala Val Ser Ala Gly Trp
 85 90 95
 Asn Gly Thr Leu Ala Pro Asn Ala Ser Ala Thr Phe Gly Phe Gln Ala
 100 105 110
 Asn Gly Ser Ala Gly Ala Pro Lys Val Asn Gly Ser Leu Cys Gly Thr
 115 120 125
 Asn Thr Ser Ser Thr Pro Ala Ser Ser Ser Val Ala Ser Ser Val Lys
 130 135 140
 Ser Ser Ala Pro Val Ser Ser Ser Ser Arg Ser Ser Ser Ser Ile Ala
 145 150 155 160
 Ile Thr Ser Ser Ser Leu Ala Arg Ser Ser Ile Ala Ser Ser Ser Ser
 165 170 175
 Leu Val Ser Ser Ser Arg Ala Ser Ser Ser Ala Pro Ser Val Phe Ser
 180 185 190
 Phe Thr Ile Gln Glu Glu Gln Ala Gly Phe Cys Arg Val Asp Gly Ile
 195 200 205
 Ala Thr Glu Ser Thr Asn Thr Gly Phe Thr Gly Asn Gly Tyr Thr Asn
 210 215 220
 Ala Asn Asn Ala Gln Gly Ala Ala Ile Glu Trp Ala Val Ser Ala Pro
 225 230 235 240
 Ser Ser Gly Arg Tyr Thr Val Ala Phe Arg Phe Ala Asn Gly Gly Thr
 245 250 255
 Ala Ala Arg Asn Gly Ser Leu Leu Ile Asn Gly Gly Ser Asn Gly Asn
 260 265 270

Tyr	Thr	Val	Glu	Leu	Pro	Leu	Thr	Gly	Ala	Trp	Ala	Thr	Trp	Gln	Ile
		275					280					285			
Ala	Ser	Val	Glu	Ile	Asp	Leu	Val	Gln	Gly	Asn	Asn	Ile	Leu	Lys	Leu
		290				295					300				
Ser	Ala	Leu	Thr	Ala	Asp	Gly	Leu	Ala	Asn	Ile	Asp	Ser	Leu	Lys	Ile
305					310					315					320
Asp	Gly	Ala	Gln	Thr	Lys	Ala	Gly	Thr	Cys	Ser	Thr	Thr	Ser	Ser	Ser
				325					330					335	
Ser	Val	Ala	Ser	Ser	Ser	Ser	Ser	Val	Lys	Ser	Ser	Ala	Ser	Ser	Ser
		340						345					350		
Ser	Ser	Ser	Ser	Thr	Ala	Ala	Lys	Ile	Leu	Thr	Leu	Asp	Gly	Asn	Pro
		355					360					365			
Ala	Ala	Ser	Trp	Phe	Asn	Lys	Ser	Arg	Thr	Lys	Trp	Asn	Ser	Ser	Arg
		370				375					380				
Ala	Asp	Ile	Val	Leu	Ser	Tyr	Gln	Gln	Ser	Asn	Gly	Gly	Trp	Pro	Lys
385						390				395					400
Asn	Leu	Asp	Tyr	Asn	Ser	Val	Ser	Ala	Gly	Asn	Gly	Gly	Ser	Asp	Ser
				405					410					415	
Gly	Thr	Ile	Asp	Asn	Gly	Ala	Thr	Ile	Thr	Glu	Met	Val	Tyr	Leu	Ala
		420						425						430	
Glu	Ile	Tyr	Lys	Asn	Gly	Gly	Asn	Thr	Lys	Tyr	Arg	Asp	Ala	Val	Arg
		435					440					445			
Arg	Ala	Ala	Asn	Phe	Leu	Val	Ser	Ser	Gln	Tyr	Ser	Thr	Gly	Ala	Leu
		450				455					460				
Pro	Gln	Phe	Tyr	Pro	Leu	Lys	Gly	Gly	Tyr	Ala	Asp	His	Ala	Thr	Phe
465						470				475					480
Asn	Asp	Asn	Gly	Met	Ala	Tyr	Ala	Leu	Thr	Val	Leu	Asp	Phe	Ala	Val
				485					490					495	
Asn	Lys	Arg	Ala	Pro	Phe	Asp	Asn	Asp	Ile	Phe	Ser	Asp	Ser	Asp	Arg
			500					505					510		
Ala	Lys	Phe	Lys	Thr	Ala	Val	Ala	Lys	Gly	Val	Asp	Tyr	Ile	Leu	Lys
		515					520					525			
Ala	Gln	Trp	Lys	Gln	Asn	Gly	Lys	Leu	Thr	Ala	Trp	Cys	Ala	Gln	His
		530				535					540				
Gly	Ala	Thr	Asp	Tyr	Gln	Pro	Lys	Lys	Ala	Arg	Ala	Tyr	Glu	Leu	Glu
545						550				555					560
Ser	Leu	Ser	Gly	Ser	Glu	Ser	Val	Gly	Ile	Leu	Ala	Phe	Leu	Met	Thr
				565					570					575	
Gln	Pro	Gln	Thr	Ala	Gln	Ile	Glu	Ala	Ala	Val	Lys	Ala	Gly	Val	Asn
			580					585						590	
Trp	Phe	Ala	Ser	Pro	Asn	Thr	Tyr	Leu	Ala	Asn	Tyr	Thr	Tyr	Asp	Ser
		595					600						605		
Ser	Lys	Ala	Ser	Thr	Asn	Pro	Ile	Val	Tyr	Lys	Ser	Gly	Ser	Arg	Met
		610				615					620				
Trp	Tyr	Arg	Phe	Tyr	Asp	Leu	Asn	Thr	Asn	Arg	Gly	Phe	Phe	Ser	Asp
625					630					635					640
Arg	Asp	Gly	Ser	Lys	Phe	Tyr	Asp	Ile	Thr	Gln	Met	Ser	Glu	Glu	Arg
				645					650					655	
Arg	Thr	Gly	Tyr	Ser	Trp	Gly	Gly	Ser	Tyr	Gly	Glu	Ser	Ile	Ile	Ser
			660				665						670		
Phe	Ala	Gln	Lys	Val	Gly	Tyr	Leu								
		675					680								

<210> 79

<211> 1746

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 79

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gctccgcggt taattgcggt cggcgaggag gcaagtcggt gggaaacgat gatgccttcg      120
atcctcgcac gcatcacacc acctcgtttt ccgaaacgca ccttctatct caatcgattc      180
ggcgccaagg gcgatggagt cacagactgc accgcggctt ttcacgcgcg gatcgatgaa      240
tgcaccaaag ccggcggttg gaaagtcgtc gtgcggcgcg gcacttatct caccggcgcg      300
attcatttga agagcaacgt caacctcgaa gtctcggaag gcgcgacgat caagttcagt      360
caggaccgca aacactacct gcctgttgtc ttctcggtt gggaagggtg cgaagtcttc      420
aactactcgc ctttcattta cgcgttcgaa cagcgaaaca tcgcgatcac cggcaaaggc      480
acgctcgacg gacagagtga ttcggaacac tgggtggcgt ggaacggccg tccgcagtac      540
ggatggaatg aagggatgaa acagcagcgt cccgatcgca acgcgttggt cacaatggcg      600
gagaaaggcg tgcgggtgcg cgagcgcacg tttggcgaag gtcattattt gaggccgcag      660
ttcattcagc cgtaccgctg ccagaacgtg ctgatccagg gcgtgacgat tcggaactcg      720
ccgatgtggg agattcatcc ggtgttggtc cgcaacgtga ctattcacga cgtgcacatc      780
gatagtcatg gaccaaaaca cgacggctgc aatcccgaat cgtgcagcga cgtgttgatt      840
aaggatagct acttcgatac cggcgacgac tgcacgcga tcaaatacgg acgcaacgcc      900
gacgggcgcg ggcttaaagc gccgactgag aacatcatcg ttcaaggatg tcgcatgaaa      960
gacggccacg gtggaatcac ggtcggcagc gagatctcgg gcggcggtgc aaacctgttt     1020
gccgagaatt gccggctcga cagtccaaac ctcgatcacg ccctgcgcgt gaagaacaat     1080
gccatgcgcg gcggattact cgagaacttc cacttccgta acatcgaagt cgggcagggtg     1140
gcccattgcc tgattacgat cgacttcaac tacgaagagg gcgcgaaagg gtcgttcacg     1200
ccggtcgttc gcgattacac ggtcgcgcgt ttgcgcagca cgaagagcaa gcacgcactc     1260
gacgtccagg gtctgcccgg cgcgcgggtc atcaacctgc gattgacaaa ctgcacattc     1320
aacgatgtgc agcaaccgaa cattctcaag aacgtcgaac aatcaacctt tgagaacgtc     1380
acgattaacg gaaagacgat cacacaaaca ggatccatct cagaaagagc ggccacgaca     1440
gcaatgaccg cgctttggcg cgacgcgtcg aggaaagaaa acggttatcc cgcgaagtgg     1500
acctatgatc atgggctggt cctgaaagga atcgagcgcg tttggaacaa taccggcgat     1560
aagaagtatc tgaagttcat ccaggacagc atggaccact tcgtcaacga cgacggctcc     1620
attcgcacct acacgatcga cgagtacaac atcgatcacg ttcttcccgg acgaaacctc     1680
ctgttccttt acaaaactac cggtcaggaa aagtatcgca aagccgccgc gttcttgcg      1740
gaacaa

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<210> 80

<211> 582

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(28)

<221> DOMAIN

<222> (81)...(458)

<223> Catalytic domain

<400> 80

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          20          25          30
Pro Trp Glu Thr Met Met Pro Ser Ile Leu Ala Arg Ile Thr Pro Pro
          35          40          45
Arg Phe Pro Lys Arg Thr Phe Tyr Leu Asn Arg Phe Gly Ala Lys Gly
          50          55          60
Asp Gly Val Thr Asp Cys Thr Ala Ala Phe His Arg Ala Ile Asp Glu

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65					70					75				80
Cys	Thr	Lys	Ala	Gly	Gly	Lys	Val	Val	Val	Pro	Ala	Gly	Thr	Tyr
				85					90				95	
Leu	Thr	Gly	Ala	Ile	His	Leu	Lys	Ser	Asn	Val	Asn	Leu	Glu	Val
			100					105					110	
Glu	Gly	Ala	Thr	Ile	Lys	Phe	Ser	Gln	Asp	Pro	Lys	His	Tyr	Leu
		115					120					125		Pro
Val	Val	Phe	Ser	Arg	Trp	Glu	Gly	Val	Glu	Val	Phe	Asn	Tyr	Ser
	130					135					140			Pro
Phe	Ile	Tyr	Ala	Phe	Glu	Gln	Arg	Asn	Ile	Ala	Ile	Thr	Gly	Lys
145					150					155				160
Thr	Leu	Asp	Gly	Gln	Ser	Asp	Ser	Glu	His	Trp	Trp	Pro	Trp	Asn
			165						170					175
Arg	Pro	Gln	Tyr	Gly	Trp	Asn	Glu	Gly	Met	Lys	Gln	Gln	Arg	Pro
			180					185					190	Asp
Arg	Asn	Ala	Leu	Phe	Thr	Met	Ala	Glu	Lys	Gly	Val	Pro	Val	Arg
		195					200					205		Glu
Arg	Ile	Phe	Gly	Glu	Gly	His	Tyr	Leu	Arg	Pro	Gln	Phe	Ile	Gln
	210					215					220			Pro
Tyr	Arg	Cys	Gln	Asn	Val	Leu	Ile	Gln	Gly	Val	Thr	Ile	Arg	Asn
225				230						235				240
Pro	Met	Trp	Glu	Ile	His	Pro	Val	Leu	Cys	Arg	Asn	Val	Thr	Ile
			245						250					255
Asp	Val	His	Ile	Asp	Ser	His	Gly	Pro	Asn	Asn	Asp	Gly	Cys	Asn
		260					265					270		Pro
Glu	Ser	Cys	Ser	Asp	Val	Leu	Ile	Lys	Asp	Ser	Tyr	Phe	Asp	Thr
	275					280						285		Gly
Asp	Asp	Cys	Ile	Ala	Ile	Lys	Ser	Gly	Arg	Asn	Ala	Asp	Gly	Arg
290					295					300				Arg
Leu	Lys	Ala	Pro	Thr	Glu	Asn	Ile	Ile	Val	Gln	Gly	Cys	Arg	Met
305				310						315				Lys
Asp	Gly	His	Gly	Gly	Ile	Thr	Val	Gly	Ser	Glu	Ile	Ser	Gly	Gly
			325					330					335	Val
Arg	Asn	Leu	Phe	Ala	Glu	Asn	Cys	Arg	Leu	Asp	Ser	Pro	Asn	Leu
		340					345						350	Asp
His	Ala	Leu	Arg	Val	Lys	Asn	Asn	Ala	Met	Arg	Gly	Gly	Leu	Leu
	355					360						365		Glu
Asn	Phe	His	Phe	Arg	Asn	Ile	Glu	Val	Gly	Gln	Val	Ala	His	Ala
	370				375						380			Val
Ile	Thr	Ile	Asp	Phe	Asn	Tyr	Glu	Glu	Gly	Ala	Lys	Gly	Ser	Phe
385				390					395					400
Pro	Val	Val	Arg	Asp	Tyr	Thr	Val	Asp	Arg	Leu	Arg	Ser	Thr	Lys
			405					410					415	Ser
Lys	His	Ala	Leu	Asp	Val	Gln	Gly	Leu	Pro	Gly	Ala	Pro	Val	Ile
		420					425						430	Asn
Leu	Arg	Leu	Thr	Asn	Cys	Thr	Phe	Asn	Asp	Val	Gln	Gln	Pro	Asn
	435					440						445		Ile
Leu	Lys	Asn	Val	Glu	Gln	Ser	Thr	Phe	Glu	Asn	Val	Thr	Ile	Asn
	450				455					460				Gly
Lys	Thr	Ile	Thr	Gln	Thr	Gly	Ser	Ile	Ser	Glu	Arg	Ala	Ala	Thr
465				470					475					480
Ala	Met	Thr	Ala	Leu	Trp	Arg	Asp	Ala	Ser	Arg	Lys	Glu	Asn	Gly
			485					490					495	Tyr
Pro	Ala	Lys	Trp	Thr	Tyr	Asp	His	Gly	Leu	Val	Leu	Lys	Gly	Ile
		500					505						510	Glu
Arg	Val	Trp	Asn	Asn	Thr	Gly	Asp	Lys	Lys	Tyr	Leu	Lys	Phe	Ile
	515					520						525		Gln
Asp	Ser	Met	Asp	His	Phe	Val	Asn	Asp	Asp	Gly	Ser	Ile	Arg	Thr
	530					535					540			Tyr

Thr Ile Asp Glu Tyr Asn Ile Asp His Val Leu Pro Gly Arg Asn Leu
 545 550 555 560
 Leu Phe Leu Tyr Lys Thr Thr Gly Gln Glu Lys Tyr Arg Lys Ala Ala
 565 570 575
 Ala Phe Leu Arg Glu Gln
 580

<210> 81
 <211> 1065
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 81
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 gcctgcgcgg gcgtgcggt atccgcggca gcgaccgacc cggtcgccga gaacatgctg 120
 ctgctgcaga ccgcctccgg tggctggtcc aagcactacc gcgggaagaa ggtcgactac 180
 acgcgaatt acgacaccgc cgagcgcgcc gcgtgcgcgc cgcccgcccg gcatgacgac 240
 gcgacgatcg acaacaaggc cacgaccagc gagatcgctt acctgggtgca ggcacatgcc 300
 aggacgggca acccggcgta cctcgacggt gcccgccgcg gggtcgaata cctgctgcgc 360
 gcgcagttacc cgaatggtgg ctggccgcag ttctaccccg accactcgtc ctaccggcac 420
 cagatcacgc tcaacgacga cgcgatggtg catgccatca ccgtgctgca ggacatcgcc 480
 gccggccgcg acggcatgca ggcgttgacg cccgagttcg gcgtccgcgc cgccgcgcgc 540
 gcgcagcgcg gcatcggaac cctgctcgag ttgcaggtgc ggatcgacgg cgagccgacc 600
 atctggggccg cgagtagca cgagcatagc ctgcagccgg ccaaggcccg cgcctatgaa 660
 ctgccctcgc tggccgtggc cgaatcggtc ggcgtggtgc gcctgctgat gcgccagccg 720
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 cgcctgcatg acctggcgct cgaacgcgtc gacgcaccgg ccgaggaaac gggcaaggac 840
 gtgcgggtcg tgaccgggcc cggcgcctcg ctgtgggcgc gcttctacga cctggatgga 900
 cagcagcctc tgctcgtcga ccgcgacagc aagcccgtcc cgttcgccag cctgcccac 960
 gagcgccgca ccggctatgc ctggtacggc acctggccgg agaagctgct ggcgcaggaa 1020
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<210> 82
 <211> 354
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(30)

<221> DOMAIN
 <222> (31)...(354)
 <223> Catalytic domain

<400> 82
 Met Thr Leu Pro Val Val Ser Leu Arg Val Leu Leu Ala Leu Leu Ala
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 Thr Leu Pro Val Ala Cys Ala Gly Ala Ala Val Ser Ala Ala Ala Thr
 20 25 30
 Asp Pro Val Ala Glu Asn Met Leu Leu Leu Gln Thr Ala Ser Gly Gly
 35 40 45
 Trp Ser Lys His Tyr Arg Gly Lys Lys Val Asp Tyr Thr Arg Asn Tyr
 50 55 60

Asp Thr Ala Glu Arg Ala Ala Leu Arg Ala Pro Gly Arg His Asp Asp
 65 70 75 80
 Ala Thr Ile Asp Asn Lys Ala Thr Thr Ser Glu Ile Ala Tyr Leu Val
 85 90 95
 Gln Ala His Ala Arg Thr Gly Asn Pro Ala Tyr Leu Asp Gly Ala Arg
 100 105 110
 Arg Gly Val Glu Tyr Leu Leu Arg Ala Gln Tyr Pro Asn Gly Gly Trp
 115 120 125
 Pro Gln Phe Tyr Pro Asp His Ser Ser Tyr Arg His Gln Ile Thr Leu
 130 135 140
 Asn Asp Asp Ala Met Val His Ala Ile Thr Val Leu Gln Asp Ile Ala
 145 150 155 160
 Ala Gly Arg Asp Gly Met Gln Ala Leu Thr Pro Glu Phe Gly Val Arg
 165 170 175
 Ala Ala Ala Ala Ala Gln Arg Gly Ile Gly Asn Leu Leu Glu Leu Gln
 180 185 190
 Val Arg Ile Asp Gly Glu Pro Thr Ile Trp Ala Ala Gln Tyr Asp Glu
 195 200 205
 His Ser Leu Gln Pro Ala Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu
 210 215 220
 Ala Val Ala Glu Ser Val Gly Val Val Arg Leu Leu Met Arg Gln Pro
 225 230 235 240
 Arg Pro Asp Ala Arg Thr Val Ala Ala Ile Glu Ser Ala Ala Arg Trp
 245 250 255
 Leu Glu Ala His Arg Leu His Asp Leu Ala Leu Glu Arg Val Asp Ala
 260 265 270
 Pro Ala Glu Glu Thr Gly Lys Asp Val Arg Val Val Thr Arg Pro Gly
 275 280 285
 Ala Ser Leu Trp Ala Arg Phe Tyr Asp Leu Asp Gly Gln Gln Pro Leu
 290 295 300
 Phe Val Asp Arg Asp Ser Lys Pro Val Pro Phe Ala Ser Leu Pro Asn
 305 310 315 320
 Glu Arg Arg Thr Gly Tyr Ala Trp Tyr Gly Thr Trp Pro Glu Lys Leu
 325 330 335
 Leu Ala Gln Glu Leu Pro Arg Trp Arg Glu Val His Ala Ala Gly Ala
 340 345 350
 Ala Pro

<210> 83
 <211> 3618
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 83
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 gaaaaaatgg cagaaaccga cttccgggat acagggttag agaatggcca gaagtattac 180
 tatgttgat ctgccgaaac gagtagcggg gagagtgcag attcacaagc tataacggct 240
 gtgcctgtag cgccattgca agtccgacc ggcctttcag caagtcattg caatggcggg 300
 gtaaccattc attgggaatc cgtcaatggt gccgagtctt accaagtctt gcgcagtaaa 360
 caaaagggga tcggctatga agtcatcaaa aacgggtgtaa cggaaaccag ttatacagat 420
 accgggattc ccgatggcga gaagtactat tatgtcgtat ccgccaagaa cgatacagct 480
 gaaagtgcaa attcccaacc gattaacggt gctgctgtat cgacgagtgg tgtaccagcc 540
 attccaaacg gtatgaacgc tactgccggt gatggcagag ctgccttaac ctgggccgct 600
 gtatccggcg cagattccta tagcatcaag cgcggtgagt ttaacagtgg tcaatatgag 660

gtcattgcta	aaaatataca	ctctaccggt	tatcaagata	taggccttac	aaacggtgat	720
acctatgatt	atgtgatttc	cgctgtcaat	gagcaagggg	aaagtttagg	ctccgaaccc	780
atcgccggtta	ctcctgcgaa	agtaacgggt	gtagcgaaag	aaggcggaga	ctttaaaacg	840
attcaagaag	ccattgatgc	tgcacctgat	aacagtagca	aacggcatgt	tatttttata	900
aaaaatggtc	aatatcgtga	aaagcttacg	atccctaaga	gcaaaaccaa	tctgagtttt	960
gtaggggaaa	gtaaggaagg	gaccgtgctt	gtttttaatg	ataatgcaaa	tacgcctggg	1020
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tactcagatt	atgtgacctt	taatgataat	gcgatgggtc	gcgttatgag	tgtattaacg	2940
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cagattgatg	atgcattggg	ccgtgggctg	gattatatgt	taaaatcgca	aattaaggta	3060
gacggtgaag	taaccgcatg	gtgtgctcag	catgacctg	tgacgtatga	accgaaaggg	3120
gctcgtgcgt	atgaacatcc	ttcaatctct	ggttcgggaat	ctgtagggat	tgtccagtat	3180
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aacacaactg	gctactacga	aaacagagta	tacgtagaag	tcgttgggga	tcagtctaaa	3540
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<210> 84
 <211> 1205
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (268)...(556)
 <223> Pectin methyl esterase domain

<221> DOMAIN
 <222> (782)...(1164)
 <223> Catalytic domain

<400> 84
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 20 25 30
 Glu Gly Pro Tyr Gln Thr Ile Ala Glu Lys Met Ala Glu Thr Asp Phe
 35 40 45
 Arg Asp Thr Gly Leu Glu Asn Gly Gln Lys Tyr Tyr Tyr Val Val Ser
 50 55 60
 Ala Glu Thr Ser Ser Gly Glu Ser Ala Asp Ser Gln Ala Ile Thr Ala
 65 70 75 80
 Val Pro Val Ala Pro Leu Gln Ala Pro Thr Gly Leu Ser Ala Ser His
 85 90 95
 Gly Asn Gly Gly Val Thr Ile His Trp Glu Ser Val Asn Gly Ala Glu
 100 105 110
 Ser Tyr Gln Val Leu Arg Ser Lys Gln Lys Gly Ile Gly Tyr Glu Val
 115 120 125
 Ile Lys Asn Gly Val Thr Glu Thr Ser Tyr Thr Asp Thr Gly Ile Pro
 130 135 140
 Asp Gly Glu Lys Tyr Tyr Tyr Val Val Ser Ala Lys Asn Asp Thr Ala
 145 150 155 160
 Glu Ser Ala Asn Ser Gln Pro Ile Asn Gly Ala Ala Val Ser Thr Ser
 165 170 175
 Gly Val Pro Ala Ile Pro Asn Gly Met Asn Ala Thr Ala Gly Asp Gly
 180 185 190
 Arg Ala Ala Leu Thr Trp Ser Ala Val Ser Gly Ala Asp Ser Tyr Ser
 195 200 205
 Ile Lys Arg Gly Glu Phe Asn Ser Gly Gln Tyr Glu Val Ile Ala Lys
 210 215 220
 Asn Ile His Ser Thr Gly Tyr Gln Asp Ile Gly Leu Thr Asn Gly Asp
 225 230 235 240
 Thr Tyr Asp Tyr Val Ile Ser Ala Val Asn Glu Gln Gly Glu Ser Leu
 245 250 255
 Gly Ser Glu Pro Ile Ala Val Thr Pro Ala Lys Val Thr Val Val Ala
 260 265 270
 Lys Glu Gly Gly Asp Phe Lys Thr Ile Gln Glu Ala Ile Asp Ala Ala
 275 280 285
 Pro Asp Asn Ser Thr Lys Arg His Val Ile Phe Ile Lys Asn Gly Gln
 290 295 300
 Tyr Arg Glu Lys Leu Thr Ile Pro Lys Ser Lys Thr Asn Leu Ser Phe
 305 310 315 320
 Val Gly Glu Ser Lys Glu Gly Thr Val Leu Val Phe Asn Asp Asn Ala
 325 330 335
 Asn Thr Pro Gly Pro Asp Gly Lys Pro Leu Gly Thr Ser Asn Ser Ser
 340 345 350
 Ser Ile Phe Ile Tyr Ala Asn Asp Phe Ile Ala Gln Asn Leu Thr Ile
 355 360 365
 Gln Asn Asp Ser Gly Gln Gly Thr Gly Gln Ala Val Ala Ala Tyr Val
 370 375 380
 Arg Ala Asp Arg Leu Tyr Phe Glu Asn Val Gln Phe Leu Gly Tyr Gln
 385 390 395 400

Asp	Thr	Leu	Tyr	Ala	His	Thr	Gly	Arg	Gln	Tyr	Tyr	Lys	Asn	Cys	Tyr	405	410	415
Val	Glu	Gly	Asp	Val	Asp	Phe	Ile	Phe	Gly	Gly	Ala	Thr	Ala	Leu	Phe	420	425	430
Asp	Thr	Cys	His	Leu	His	Ser	Lys	Arg	Thr	Gly	Ser	Lys	Leu	Thr	Ala	435	440	445
Ala	Ser	Thr	Asp	Gln	Val	Thr	Pro	Tyr	Gly	Tyr	Val	Phe	Leu	Asp	Ser	450	455	460
Lys	Ile	Thr	Ser	Asp	Glu	Gly	Val	Thr	Asn	Val	His	Leu	Gly	Arg	Pro	465	470	475
Trp	Arg	Pro	Tyr	Ser	Ala	Val	Thr	Tyr	Ile	Asn	Thr	Glu	Met	Asp	Ala	485	490	495
Ser	Ile	Val	Pro	Asp	Gly	Trp	Asp	Asn	Trp	Gly	Lys	Val	Glu	Asn	Glu	500	505	510
Lys	Thr	Ala	Arg	Tyr	Ser	Glu	Tyr	Asn	Asn	Met	Gly	Pro	Gly	Ala	Asp	515	520	525
Pro	Lys	Lys	Arg	Asp	Pro	Trp	Thr	Thr	Gln	Leu	Thr	Pro	Glu	Glu	Ala	530	535	540
Asn	Gln	Tyr	Thr	Val	Gln	Asn	Val	Met	Lys	Gly	Ser	Asp	Gly	Trp	Asp	545	550	555
Pro	Glu	Arg	Ile	Gly	Ile	Ile	Pro	Leu	Ser	Pro	Leu	Ser	Ala	Pro	Ile	565	570	575
Ile	Ser	Leu	Asp	Gln	Arg	Asp	Ser	Ile	Val	Asn	Thr	Pro	Ser	Phe	Thr	580	585	590
Ile	Thr	Gly	Gln	Val	Asp	Lys	Glu	Ala	Ala	Val	Ser	Val	Asn	Gly	Lys	595	600	605
Glu	Ile	Ser	Leu	Gln	Lys	Asp	Gly	Ser	Phe	Ser	Thr	Thr	Val	Val	Leu	610	615	620
Asn	Asp	Gly	Leu	Asn	Thr	Ile	Thr	Val	Gly	Ala	Val	Asp	Ala	Ala	Gly	625	630	635
Asn	Gln	Ala	Ile	Pro	Ala	Val	Leu	Lys	Ile	Val	Tyr	Asp	His	Glu	Lys	645	650	655
Pro	Val	Val	Ser	Ile	Asp	Asp	Leu	Lys	Gly	Glu	Lys	Asn	Gly	Asn	His	660	665	670
Tyr	Asn	Val	Ile	Tyr	Asn	Pro	Leu	Pro	Ile	Thr	Gly	Lys	Leu	Asn	Glu	675	680	685
Ala	Gly	Thr	Val	Met	Val	Asn	Gly	Glu	Lys	Val	Asn	Val	Ser	Glu	Lys	690	695	700
Leu	Thr	Phe	Ser	Thr	Lys	Val	Ile	Leu	Lys	Pro	Gly	Leu	Asn	Asn	Ile	705	710	715
Thr	Ile	Thr	Ala	Val	Asp	Gln	Ala	Gly	Asn	Glu	Ala	Glu	Ser	Ile	Thr	725	730	735
Ile	Asn	Val	Val	Pro	Lys	Gly	Asn	Ala	Val	Pro	Asp	Gly	Pro	Val	Lys	740	745	750
Ile	Ile	Lys	Ser	Glu	Thr	Thr	Asn	Ala	Asn	Thr	Val	Glu	Val	Thr	Phe	755	760	765
Asn	Ser	Lys	Leu	Glu	Lys	Phe	Asp	Ser	Ser	Asp	Ile	Ala	Leu	Gln	Thr	770	775	780
Ala	Thr	Asn	Val	Trp	Ala	Ala	Leu	Asn	Pro	Gly	Leu	Lys	Gln	Leu	Met	785	790	795
Thr	Val	Glu	Ser	Ile	Thr	Thr	Lys	Val	Asn	Lys	Asp	Asn	Gln	Thr	Val	805	810	815
Ala	Val	Ile	Lys	Thr	Lys	Glu	Ala	Phe	Gln	Glu	Asp	Gly	Thr	Ile	Thr	820	825	830
Leu	Pro	Lys	Val	Glu	Asp	Pro	Phe	His	Ile	Gln	Tyr	Leu	Asn	Ala	Asp	835	840	845
Tyr	Tyr	Thr	Gly	Asp	Arg	Thr	Gln	Asp	Ile	Lys	His	Ala	Asp	Ala	Leu	850	855	860
Leu	Thr	Trp	Gln	Met	Asp	His	Gly	Gly	Trp	Phe	Lys	Asn	Trp	Val	Glu			

865		870		875		880
Lys Tyr Lys Arg	Pro Trp Asp Gly Lys Glu Pro Lys Ser Glu Trp Tyr					
	885		890			895
Ser Thr Asn His	Gly Glu Leu Gly Thr Ile Asp Asn Asp Ala Thr Thr					
	900		905			910
Asn Glu Ile Leu Phe	Leu Ala Leu Met Tyr Lys Glu Thr Gly Asp Ala					
	915		920			925
Arg Tyr Lys Asp Ser Val	Leu Lys Gly Ile Asp Phe Leu Leu Glu Met					
	930		935			940
Gln Val Asp Ser Gly Gly	Trp Pro Gln Val Tyr Pro Ala Arg Ser Gly					
	945		950			955
Tyr Ser Asp Tyr Val Thr	Phe Asn Asp Asn Ala Met Val Arg Val Met					
	965		970			975
Ser Val Leu Thr Met Val	Lys Glu Lys Lys Tyr Pro Phe Asn Ser Asn					
	980		985			990
Leu Gly Asp Glu Gln Leu	Ser Glu Gln Ile Asp Asp Ala Leu Gly Arg					
	995		1000			1005
Gly Leu Asp Tyr Met Leu	Lys Ser Gln Ile Lys Val Asp Gly Glu Val					
	1010		1015			1020
Thr Ala Trp Cys Ala Gln	His Asp Pro Val Thr Tyr Glu Pro Lys Gly					
	1025		1030			1035
Ala Arg Ala Tyr Glu His	Pro Ser Ile Ser Gly Ser Glu Ser Val Gly					
	1045		1050			1055
Ile Val Gln Tyr Leu Met	Ser Leu Pro Asn Pro Ser Thr Glu Val Gln					
	1060		1065			1070
Ala Ala Ile His Gly Ala	Leu Asn Trp Phe Glu Glu Ala Lys Leu Ala					
	1075		1080			1085
Gly Thr Lys Tyr Val Ser	Gly Asp Pro Asn Gly Gln Tyr Phe Tyr Pro					
	1090		1095			1100
Asp Ala Asn Ser Asn Thr	Trp Tyr Arg Phe Tyr Glu Ile Gly Thr Asn					
	1105		1110			1115
Arg Pro Ile Phe Ser Gly	Arg Asp Gly Val Ile Lys His Asn Ile Leu					
	1125		1130			1135
Glu Ile Glu Lys Glu Arg	Arg Asp Gly Tyr Arg Trp Ala Gly Glu Trp					
	1140		1145			1150
Pro Gln Lys Leu Leu Asn	Ile Ala Asn Thr Thr Gly Tyr Tyr Glu Asn					
	1155		1160			1165
Arg Val Tyr Val Glu Val	Val Gly Asp Gln Ser Lys Asn Ala Ala Gly					
	1170		1175			1180
Glu Ser Leu Glu Ile Gly	Asn Leu Tyr Arg Ile Glu Ala Ser Ala Ser					
	1185		1190			1195
Gly Ser Thr Ser Lys						1200
	1205					

<210> 85

<211> 1152

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 85

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tctaagaaaa atgatcagga agtcggcgcg atcgcgtgga aagatgcaca tggaaagccg	180
gatgagtgg atgcgagtgt tgaggcactg cggatggccg ataacgtcgt tctctatcaa	240
cgcgactcag gtggttgccc caagaacatc gacatggcga aggcactcaa cgatcgtgag	300
caggctgcga tctctcccca gaagaaaaag aacgactcca cgatcgacaa tgggtgcgact	360

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cacacacagt tatectttct ggcgcgcgtc tatacagcac agcgtcagga gcgacatcgc 420
gagtcgtttt tcaaaggatt ggattactta ctgaatgcgc agtatccaaa tggaggctgg 480
ccgcagtttt atccgaaccc gacgggctat cacaagcaca ttacttacia cgacggtgcg 540
atgattggtg tgatgaaggt gctgcgcgat atcgtcgcgc cgaagccttt gtacgctttt 600
gtcgacgaag ctgggcgcgc gaaggcgacg agtgcagttg aaaaagggat cgagtgcatt 660
ttgaaaacgc aggtggtggt agatgggcgt cgcactgtgt ggagtgcgca acatgatgaa 720
gtaacgttag cgccagctcc tgcgcgaacc ttcgagttaa cttcgttgag cggcgggtgag 780
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acatctctgt ga 1152

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<210> 86

<211> 383

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (1)...(383)

<223> Catalytic domain

<400> 86

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Lys Gln Leu Ser Gly Val Glu Ala Lys Leu Phe Gln Arg Glu Arg Phe
20          25          30
Phe Ser Leu Ala Ala Glu His Thr Ser Lys Lys Asn Asp Gln Glu Val
35          40          45
Gly Ala Ile Ala Trp Lys Asp Ala His Gly Lys Pro Asp Glu Trp Tyr
50          55          60
Ala Ser Val Glu Ala Leu Arg Met Ala Asp Asn Val Val Leu Tyr Gln
65          70          75          80
Arg Asp Ser Gly Gly Trp Pro Lys Asn Ile Asp Met Ala Lys Ala Leu
85          90          95
Asn Asp Arg Glu Gln Ala Ala Ile Leu Arg Gln Lys Lys Lys Asn Asp
100         105         110
Ser Thr Ile Asp Asn Gly Ala Thr His Thr Gln Leu Ser Phe Leu Ala
115         120         125
Arg Val Tyr Thr Ala Gln Arg Gln Glu Arg His Arg Glu Ser Phe Phe
130         135         140
Lys Gly Leu Asp Tyr Leu Leu Asn Ala Gln Tyr Pro Asn Gly Gly Trp
145         150         155         160
Pro Gln Phe Tyr Pro Asn Pro Thr Gly Tyr His Lys His Ile Thr Tyr
165         170         175
Asn Asp Gly Ala Met Ile Gly Val Met Lys Val Leu Arg Asp Ile Ala
180         185         190
Ala Ala Lys Pro Leu Tyr Ala Phe Val Asp Glu Ala Arg Arg Ala Lys
195         200         205
Ala Thr Ser Ala Val Glu Lys Gly Ile Glu Cys Ile Leu Lys Thr Gln
210         215         220
Val Val Val Asp Gly Arg Arg Thr Val Trp Ser Ala Gln His Asp Glu
225         230         235         240
Val Thr Leu Ala Pro Ala Pro Ala Arg Thr Phe Glu Leu Thr Ser Leu

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				245					250					255	
Ser	Gly	Gly	Glu	Ser	Val	Asp	Ile	Val	Arg	Phe	Leu	Met	Ser	Ile	Lys
			260					265					270		
Asp	Pro	Ser	Pro	Lys	Val	Val	Asp	Ala	Val	Glu	Ser	Ala	Val	Lys	Trp
			275				280					285			
Phe	Glu	Gln	Ser	Glu	Leu	Lys	Gly	Val	Lys	Trp	Val	Lys	Lys	Ala	Asp
			290				295				300				
Ala	Ser	Lys	Pro	Gly	Gly	Phe	Asp	Cys	Val	Val	Val	Lys	Asp	Pro	Glu
305					310					315					320
Ser	Ser	Val	Trp	Ala	Arg	Phe	Tyr	Glu	Ile	Gly	Thr	Asn	Arg	Pro	Ile
				325					330					335	
Phe	Ser	Gly	Arg	Asp	Gly	Val	Val	Lys	Tyr	Asp	Val	Ala	Gln	Ile	Glu
			340					345					350		
His	Glu	Arg	Arg	Thr	Asn	Tyr	Glu	Trp	Tyr	Val	Asp	Glu	Ala	Ala	Lys
			355				360					365			
Leu	Leu	Lys	Lys	Glu	Tyr	Pro	Ala	Trp	Arg	Lys	Arg	Thr	Ser	Leu	
			370			375					380				

<210>	87
<211>	1698
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

[illegible]

$\langle 210 \rangle$	88
$\langle 211 \rangle$	565

<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(32)

<221> DOMAIN
<222> (33)...(375)
<223> Catalytic domain

<400> 88
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Ala Ala Thr Gly Gly Phe Ser Thr Thr Asp Gly Gly Ala Ala Ser Gly
35 40 45
Ser Gln Ser Phe Thr Ala Ala Asn Leu Asp Gln Leu Asn Thr Ile Val
50 55 60
Ala Asn Ala Lys Ser Gly Gly Tyr Pro Val Val Ile Thr Tyr Thr Gly
65 70 75 80
Asn Glu Asp Ser Leu Ile Asn Gln Met Ile Lys Asp His Thr Val Asp
85 90 95
Ser Ser Gly Asn Cys Pro Asn Pro Arg Trp Ser Glu Thr Tyr Arg Lys
100 105 110
Val Glu Ile Lys Glu Met Thr Lys Gly Val Thr Ile Ile Gly Ala Asn
115 120 125
Gly Ser Ser Ala Asn Phe Gly Ile Val Val Asn Lys Ser Ser Asn Val
130 135 140
Ile Ile Arg Asn Met Lys Ile Gly Ala Leu Ala Gly Ala Ser Asn Asp
145 150 155 160
Ala Asp Met Ile Arg Ile Asp Ser Gly Thr Asn Val Trp Val Asp His
165 170 175
Asn Glu Leu Phe Ala Val Asn Asn Glu Cys Lys Gly Ser Pro Asp Gly
180 185 190
Asp Leu Thr Phe Glu Ser Ala Ile Asp Ile Lys Lys Asp Ser His Asn
195 200 205
Ile Thr Val Ser Tyr Asn Leu Ile Arg Asp Ser Lys Lys Val Gly Leu
210 215 220
Asp Gly Ser Ser Ser Ser Asp Ile Ala Gly Gly Arg Glu Ile Thr Phe
225 230 235 240
His His Asn Ile Tyr Lys Asn Val Asn Ala Arg Leu Pro Leu Gln Arg
245 250 255
Gly Gly Trp Thr His Met Tyr Asn Asn Leu Tyr Asp Gly Ile Thr Gly
260 265 270
Ser Gly Ile Asn Val Arg Gln Ala Gly Tyr Ala Leu Ile Glu Ser Asn
275 280 285
Trp Phe Gln Asn Ala Val Asn Pro Val Thr Cys Arg Tyr Asp Ser Ser
290 295 300
Asn Cys Gly Phe Trp Asp Leu Arg Asn Asn Asn Val Lys Ser Pro Ala
305 310 315 320
Asp Phe Ala Thr Tyr Asn Ile Thr Trp Thr Ser Gly Gly Thr Ile Asp
325 330 335
Ala Thr Asn Trp Thr Thr Thr Ala Pro Phe Pro Ile Ser Ile Pro Tyr
340 345 350
Ser Tyr Ser Pro Val Ser Pro Gln Cys Val Lys Asp Lys Leu Ala Ser

355	360	365
Val Ala Gly Val Gly Lys Asn Gly Ala Val Leu Asn Ser Ser Val Cys		
370	375	380
Gly Gly Ser Ser Ser Val Pro Ser Ser Ser Val Ala Thr Thr Ser		
385	390	395
Lys Ser Ser Ser Ser Val Ala Thr Ser Lys Ser Ser Ser Val Ala Thr		400
405	410	415
Thr Ser Ser Lys Ser Ser Ser Ser Val Val Pro Ser Ser Ser Ser		
420	425	430
Ser Ser Val Val Asn Asn Gly Ser Ile Ala Leu Thr Ala Thr Ala Thr		
435	440	445
Gly Asn Ser Ile Val Leu Ser Trp Ser Pro Asn Asn Leu Thr Leu Gly		
450	455	460
Thr Gln Glu Val Tyr Arg Asp Thr Asp Ser Asp Pro Ser Gly Arg Val		
465	470	475
Arg Ile Ala Ala Leu Ser Ser Ser Thr Arg Met Tyr Thr Asp Ala Thr		480
485	490	495
Ala Ser Ala Gly Gln Thr Phe Tyr Tyr Trp Ile Lys Asn Thr Thr Asn		
500	505	510
Gly Val Thr Thr Asn Ser Asn Ala Ala Ser Ala Ala Ile Gly Asp Ala		
515	520	525
Ala Arg Ala Ile Arg Ala Cys Ala Gly Asn Arg Gly Ser Gly Ala Arg		
530	535	540
Thr Ser Arg Ala Val Ser Thr Gly Ser Asn Pro Arg Gly Pro Ala Gly		
545	550	555
Ser His Pro Arg Ala		560
565		

<210> 89

<211> 1377

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 89

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atcctcgaac	gcatacaagg	accgcgtttt	ccgaaacgca	cgtgctatct	caaccggttt	180
ggagcaaaag	gcgacgggca	aactgattgc	acttcagctt	ttcgacgcgc	aatcgatcag	240
tggtcgaag	cgggcggttg	caaagtgtgc	gttccgcagg	gaatgtatct	caccggcgca	300
attcacttga	agagcaacgt	caatctcgag	atctccgaag	gcgcgacgat	caagttcagt	360
caaaacccga	aagactatct	cccgtgtggt	ttttcgcggt	gggaaggcgt	cgaagtattc	420
aactactcac	ctttcatcta	cgcatttgaa	cagcagaaca	tcgcgatcac	gggcaagggc	480
acgctcgatg	ggcagagtga	taacgaacac	tggtggccat	ggaacggacg	cgccagggtac	540
ggttggaag	aagggatgag	ccaccagcgt	ccggatcgaa	acgcgctctt	tgcatggcg	600
gaaaaagggtg	tttcggttcg	cgaacgtggt	ttcggcgagg	gtcattactt	aaggccgcag	660
ttcattcagc	cgtatcgctg	ccagaacgta	ttgatcgacg	gagttacgat	acgaaactcg	720
ccgatgtggg	aaattcatcc	ggtgctgtgc	cggaatgtca	tcgtgcaaaa	cgtgcacatt	780
aacagtcgatg	gaccaaacia	cgatggctgc	aatcccgaag	cgtgcactga	tgtgctgatt	840
aagaactgtt	acttcgacac	tggcgacgac	tgtatcgcgg	tcaaatcagg	acgcaacgcg	900
gacggccggc	ggcttaaagc	gccgacagag	aacgtgatcg	tgcaagactg	tcaaatgaaa	960
gatggacacg	gcgggatcac	tgctggcagt	gagatctcag	gcggtgtgag	aaatctgttt	1020
gcggagaact	gccggcttga	tagtccaaac	ctggaccatg	ctttgcgggt	taagaacaac	1080
gcgatgcgtg	gagggctgct	cgagaatttg	cacttccgaa	acatcgaaag	tggtcaggtg	1140
gcgcatgcag	tgatcacgat	cgattttaat	tacgaggaag	gcgcgaaagg	atcgttcacg	1200
ccggtggttc	gtgactacac	tgctgatggg	ttgcgcagca	cgcgaaagcaa	atagcgctc	1260
gacgttcaag	gtctgtcggg	cgcgccgatc	gtaaatctgc	gtctgacgaa	ttgcacgttc	1320

gacaatgttg ccgaaggga cgtcgtgaag aatgttaagg acgcgacaat tcaaaaa

1377

<210> 90
<211> 459
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(31)

<221> DOMAIN
<222> (32)...(459)
<223> Catalytic domain

<400> 90
Met Thr Thr Arg Arg Glu Phe Ile Arg Asp Leu Leu Val Gly Gly Val
1 5 10 15
Val Val Ala Val Ala Pro Arg Phe Leu Ala Phe Ser Ser Val Ala Ser
20 25 30
Pro Trp Glu Thr Val Met Pro Ser Ile Leu Glu Arg Ile Lys Pro Pro
35 40 45
Arg Phe Pro Lys Arg Thr Cys Tyr Leu Asn Arg Phe Gly Ala Lys Gly
50 55 60
Asp Gly Gln Thr Asp Cys Thr Ser Ala Phe Arg Arg Ala Ile Asp Gln
65 70 75 80
Cys Ser Lys Ala Gly Gly Gly Lys Val Ile Val Pro Gln Gly Met Tyr
85 90 95
Leu Thr Gly Ala Ile His Leu Lys Ser Asn Val Asn Leu Glu Ile Ser
100 105 110
Glu Gly Ala Thr Ile Lys Phe Ser Gln Asn Pro Lys Asp Tyr Leu Pro
115 120 125
Val Val Phe Ser Arg Trp Glu Gly Val Glu Val Phe Asn Tyr Ser Pro
130 135 140
Phe Ile Tyr Ala Phe Glu Gln Gln Asn Ile Ala Ile Thr Gly Lys Gly
145 150 155 160
Thr Leu Asp Gly Gln Ser Asp Asn Glu His Trp Trp Pro Trp Asn Gly
165 170 175
Arg Ala Arg Tyr Gly Trp Lys Glu Gly Met Ser His Gln Arg Pro Asp
180 185 190
Arg Asn Ala Leu Phe Ala Met Ala Glu Lys Gly Val Ser Val Arg Glu
195 200 205
Arg Val Phe Gly Glu Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro
210 215 220
Tyr Arg Cys Gln Asn Val Leu Ile Asp Gly Val Thr Ile Arg Asn Ser
225 230 235 240
Pro Met Trp Glu Ile His Pro Val Leu Cys Arg Asn Val Ile Val Gln
245 250 255
Asn Val His Ile Asn Ser His Gly Pro Asn Asn Asp Gly Cys Asn Pro
260 265 270
Glu Ser Cys Thr Asp Val Leu Ile Lys Asn Cys Tyr Phe Asp Thr Gly
275 280 285
Asp Asp Cys Ile Ala Val Lys Ser Gly Arg Asn Ala Asp Gly Arg Arg
290 295 300
Leu Lys Ala Pro Thr Glu Asn Val Ile Val Gln Asp Cys Gln Met Lys
305 310 315 320
Asp Gly His Gly Gly Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val

				325				330					335		
Arg	Asn	Leu	Phe	Ala	Glu	Asn	Cys	Arg	Leu	Asp	Ser	Pro	Asn	Leu	Asp
			340					345					350		
His	Ala	Leu	Arg	Val	Lys	Asn	Asn	Ala	Met	Arg	Gly	Gly	Leu	Leu	Glu
		355					360					365			
Asn	Leu	His	Phe	Arg	Asn	Ile	Glu	Val	Gly	Gln	Val	Ala	His	Ala	Val
	370					375					380				
Ile	Thr	Ile	Asp	Phe	Asn	Tyr	Glu	Glu	Gly	Ala	Lys	Gly	Ser	Phe	Thr
385					390					395					400
Pro	Val	Val	Arg	Asp	Tyr	Thr	Val	Asp	Gly	Leu	Arg	Ser	Thr	Arg	Ser
			405						410					415	
Lys	Tyr	Ala	Leu	Asp	Val	Gln	Gly	Leu	Ser	Gly	Ala	Pro	Ile	Val	Asn
		420						425					430		
Leu	Arg	Leu	Thr	Asn	Cys	Thr	Phe	Asp	Asn	Val	Ala	Glu	Gly	Asn	Val
		435					440					445			
Val	Lys	Asn	Val	Lys	Asp	Ala	Thr	Ile	Gln	Lys					
	450					455									

<210>	91
<211>	1125
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<400>	91						
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tggagcgcac	ccctagtgcca	gcgggcccgaa	tggtacggga	gtgacgaagc	gatccgcac		180
gcggacaacg	tcctcctcta	ccagcgcaac	accggcgggt	ggccgaagga	catagatatg		240
gccgagccca	tcccgggaaca	caggaagtcc	tttttctca	ccgagaagga	gcggaccgat		300
gactcgacca	tcgacaacgg	tgccaccgtg	accagctca	agtatctcgc	ccgcgtctac		360
aaggcgacca	ggctggaacg	gttcaaggag	ggcttctca	aaggtctcga	ctacctcttg		420
gccgcccagt	acccgacaacg	cggctggccc	cagtattatc	ctaaccttgag	gggctactac		480
gccaacatca	cttataacga	caatgccatg	gtgaacgtgc	tcaccctcct	ccagagcac		540
gccaaaaagc	ccccggagta	cgacttcgtc	gaccggcgcc	gccgggagaa	ggccgcccgg		600
gccgtggcga	aagggatcga	ctgcctctc	aagaccaga	tccgtgtcaa	tggaaaactt		660
accgcttggt	gcgcccagca	tgacgccaag	acgctggcgc	ccgcgccggc	ccgttcgtat		720
gagcttgagt	ccatcagcgg	tttcgagagc	gtcgggatcg	tccggttctt	aatgagcctc		780
gagaatccga	gcccgaaagt	catcgaggcg	gtagaggccg	ccgtgaaatg	gttcgaggag		840
gtcaagctta	ccgggatcaa	ggtggctcag	aaaccgcacc	cgctcccttc	ggcggttac		900
gaccgcgtgg	tgtgtcgaaga	ccccaacgcg	cgcgccatct	gggcccgggt	ctacgagatc		960
ggcaccaaac	gtcccttctt	ctgcggcgcg	gatggtatca	aaaaatacacg	cctggcgagg		1020
atcgaacacg	aacgcggggt	cggttactcc	tggtacacca	atgccccggc	ctacctcatc		1080
gagaaggagt	atccgctctg	gcggggccaaa	caccctacca	agtaa			1125

<210>	92
<211>	374
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

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<221> DOMAIN
<222> (1) ... (374)
```

<400> 92

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Met Val Leu Gly Asn Asn Gly Gly Ser Leu Ser Cys Val Gln Tyr Ile
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Val Ile Val Lys Gly Pro Gly Gly Pro Arg Pro Pro Val Lys Pro Ala
 20          25          30
Val Gln Ala Pro Val Arg Val Thr Trp Ser Ala Ser Leu Val Gln Arg
 35          40          45
Pro Glu Trp Tyr Gly Ser Asp Glu Ala Ile Arg Ile Ala Asp Asn Val
 50          55          60
Leu Leu Tyr Gln Arg Asn Thr Gly Gly Trp Pro Lys Asp Ile Asp Met
 65          70          75          80
Ala Glu Pro Ile Pro Glu His Arg Lys Ser Phe Phe Leu Thr Glu Lys
 85          90          95
Glu Arg Thr Asp Asp Ser Thr Ile Asp Asn Gly Ala Thr Val Thr Gln
100          105          110
Leu Lys Tyr Leu Ala Arg Val Tyr Lys Ala Thr Arg Leu Glu Arg Phe
115          120          125
Lys Glu Gly Phe Leu Lys Gly Leu Asp Tyr Leu Leu Ala Ala Gln Tyr
130          135          140
Pro Asn Gly Gly Trp Pro Gln Tyr Tyr Pro Asn Leu Arg Gly Tyr Tyr
145          150          155          160
Ala Asn Ile Thr Tyr Asn Asp Asn Ala Met Val Asn Val Leu Thr Leu
165          170          175
Leu Gln Ser Ile Ala Lys Lys Ala Pro Glu Tyr Asp Phe Val Asp Pro
180          185          190
Ala Arg Arg Glu Lys Ala Ala Arg Ala Val Ala Lys Gly Ile Asp Cys
195          200          205
Ile Leu Lys Thr Gln Ile Arg Val Asn Gly Lys Leu Thr Ala Trp Cys
210          215          220
Ala Gln His Asp Ala Lys Thr Leu Ala Pro Ala Pro Ala Arg Ser Tyr
225          230          235          240
Glu Leu Glu Ser Ile Ser Gly Phe Glu Ser Val Gly Ile Val Arg Phe
245          250          255
Leu Met Ser Leu Glu Asn Pro Ser Pro Lys Val Ile Glu Ala Val Glu
260          265          270
Ala Ala Val Lys Trp Phe Glu Glu Val Lys Leu Thr Gly Ile Lys Val
275          280          285
Val Glu Lys Pro Asp Pro Ser Leu Pro Gly Gly Tyr Asp Arg Val Val
290          295          300
Val Glu Asp Pro Asn Ala Pro Pro Ile Trp Ala Arg Phe Tyr Glu Ile
305          310          315          320
Gly Thr Asn Arg Pro Phe Phe Cys Gly Arg Asp Gly Ile Lys Lys Tyr
325          330          335
Ser Leu Ala Glu Ile Glu His Glu Arg Arg Val Gly Tyr Ser Trp Tyr
340          345          350
Thr Asn Ala Pro Ala Tyr Leu Ile Glu Lys Glu Tyr Pro Leu Trp Arg
355          360          365
Ala Lys His Pro Thr Lys
370

```

<210> 93

<211> 1062

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 93

gtggatccaa agaattggaa cccgaaaaaa gccgacgatt catggctcga aaagacgaaa

60

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gtcgcacgaag cgacgcgcat cgccaaccag gttttgctct ttcagcgcg taacggcggc 180
tgggaaaaaa acgtcgacat ggcggcgatg ctactcaag ccgaacgaga aaaactcgtc 240
aaagaaaaat ctcacaccga tacgaccatc gacaacggcg cgacgaccac gcagctgcgt 300
tatctggcaa aagtcacac ggcgaaaaac atcgaagctc ataaacagtc gtttctcaag 360
ggattggatt ttctgctcgc gatgcagtat gaaaacggag gatttccgca atattatcct 420
ttgaaaaacg attattcgcg cgagattact ttcaacgacg acgcgatgat caatgttctt 480
aaattgctgc gcgacgtggc aaaaaaagaag gaagattatt tattcgctcg cgaagaccgg 540
cgcgccagag cggaaggcgc ggtcgaaaaa ggctgccgcc tgatcttgaa aacacaggtc 600
gccatcgacg gcaaaaaaac gatctgggcg gcgcagtacg acgaaaacac tttgaaaccg 660
gcaaatgcga gaaagtgtga gccgcctcg ctgccttcgc gcgaatcggg cagcgtggtc 720
agatttttga tgctcgacgc caaaccgcgac gaggaaaaaa tcggagcgat cgaatcggcg 780
atcgaatggt ttcaaaaaaa caaactgagc ggcatctcgt gggaatcgaa aagcggagaa 840
aacctggtcg tcaaagacaa agcggcgccg ccgatctggg gaagggttta tcaattcgaa 900
accatgcgcc ccatttttat cgggcgcgac gcggtgattc gctacgatgt catgcaaadc 960
gaagccgaac gccgcaacgg ctacggctgg tacacgaacg agccgaacga gcttttggac 1020
aaagattatc cgaaatggaa agagaaaatt aagaaaaatt ag 1062

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<210> 94
 <211> 353
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (1)...(353)

<400> 94

Met	Asp	Pro	Lys	Asn	Trp	Asn	Pro	Lys	Lys	Ala	Asp	Asp	Ser	Trp	Leu
1			5					10					15		
Glu	Lys	Thr	Lys	Pro	Asp	Tyr	Arg	Leu	Val	Ser	Trp	Arg	Asp	Val	Leu
			20					25					30		
Asp	Gln	Thr	Gln	Leu	Trp	Tyr	Ala	Val	Asp	Glu	Ala	Thr	Arg	Ile	Ala
			35				40					45			
Asn	Gln	Val	Leu	Leu	Phe	Gln	Arg	Asp	Asn	Gly	Gly	Trp	Glu	Lys	Asn
			50			55					60				
Val	Asp	Met	Ala	Ala	Met	Leu	Thr	Gln	Ala	Glu	Arg	Glu	Lys	Leu	Val
65					70				75					80	
Lys	Glu	Lys	Ser	His	Thr	Asp	Thr	Thr	Ile	Asp	Asn	Gly	Ala	Thr	Thr
				85					90					95	
Thr	Gln	Leu	Arg	Tyr	Leu	Ala	Lys	Val	Ile	Thr	Ala	Lys	Asn	Ile	Glu
			100					105					110		
Ala	His	Lys	Gln	Ser	Phe	Leu	Lys	Gly	Leu	Asp	Phe	Leu	Leu	Ala	Met
		115					120				125				
Gln	Tyr	Glu	Asn	Gly	Gly	Phe	Pro	Gln	Tyr	Tyr	Pro	Leu	Lys	Asn	Asp
130					135						140				
Tyr	Ser	Arg	Glu	Ile	Thr	Phe	Asn	Asp	Asp	Ala	Met	Ile	Asn	Val	Leu
145					150					155					160
Lys	Leu	Leu	Arg	Asp	Val	Ala	Lys	Lys	Lys	Glu	Asp	Tyr	Leu	Phe	Val
				165					170					175	
Asp	Glu	Asp	Arg	Arg	Ala	Arg	Ala	Glu	Gly	Ala	Val	Glu	Lys	Gly	Val
			180					185					190		
Arg	Leu	Ile	Leu	Lys	Thr	Gln	Val	Ala	Ile	Asp	Gly	Lys	Lys	Thr	Ile
		195				200						205			
Trp	Ala	Ala	Gln	Tyr	Asp	Glu	Asn	Thr	Leu	Lys	Pro	Ala	Asn	Ala	Arg
210						215					220				
Lys	Phe	Glu	Pro	Ala	Ser	Leu	Ala	Ser	Arg	Glu	Ser	Val	Ser	Val	Val

225					230					235					240	
Arg	Phe	Leu	Met	Leu	Asp	Ala	Lys	Pro	Asp	Glu	Glu	Lys	Ile	Gly	Ala	
				245					250					255		
Ile	Glu	Ser	Ala	Ile	Glu	Trp	Phe	Gln	Lys	Asn	Lys	Leu	Ser	Gly	Ile	
				260					265					270		
Arg	Trp	Glu	Ser	Lys	Ser	Gly	Glu	Asn	Leu	Val	Val	Lys	Asp	Lys	Ala	
				275					280					285		
Ala	Pro	Pro	Ile	Trp	Gly	Arg	Phe	Tyr	Gln	Phe	Glu	Thr	Met	Arg	Pro	
				290					295					300		
Ile	Phe	Ile	Gly	Arg	Asp	Ala	Val	Ile	Arg	Tyr	Asp	Val	Met	Gln	Ile	
305					310					315					320	
Glu	Ala	Glu	Arg	Arg	Asn	Gly	Tyr	Gly	Trp	Tyr	Thr	Asn	Glu	Pro	Asn	
				325					330					335		
Glu	Leu	Leu	Asp	Lys	Asp	Tyr	Pro	Lys	Trp	Lys	Glu	Lys	Ile	Lys	Lys	
				340					345					350		
Asn																

<210>	95
<211>	1074
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<400>	95								
atgacgcctac	cggttgttttc	cctgcgcgcta	ctgctggcgcc	tgctggccac	gtcgcgccgtc				60
gcctgcgcgg	gcgccgcgggc	accgcgcact	gcgaccgatc	cggtcgccga	gaacatgctg				120
cttctgcaga	ccgcctccgg	cggtcgtgtcc	aagcactacc	gcgagaagaa	ggtcgactac				180
gcgcgcgact	acgacgccgc	cgagcgcgcc	gcgctgcgcg	cgcccgcacc	gcatgacgat				240
gcgacgatcg	acaacaaggc	cacgaccacc	gagatcgctt	acctggtgca	ggcacatgcc				300
aggacgggca	atccgcgccta	cctcgacggc	gcgcgcgcgc	gcgtcgagta	cctgctgcgc				360
gcccagtacc	cgaaggcgcg	ctggcgcgag	ttctaccocg	accattcgctc	ctaccggcac				420
cagatcacgc	tcaacgcagca	tgcgatggtg	cacgccatca	ccgtgctgca	ggacatcgcc				480
gcgggccgca	acggcatgca	ggtgctggcg	ccggagtctg	gcgtccgcgc	cgccgcggcc				540
gcgcagcgcg	gcatcgga aa	cctgctcgag	ttgcaggtgc	ggatcgccgg	ggtgccgacg				600
atatggggccg	cgcagtacga	cgagaccagc	ctgcaaccgg	ccaaggcccc	cgcgtagcaa				660
ctgccttcgc	tggccgtggc	cgaatcggtc	ggcgtggtgc	gcctgctgat	gcgccagccg				720
gcgcctgatg	cgcgcacggc	cgccgcgatc	gaggcgggcg	ccgactggct	ggaggcgcac				780
cgcttgccgg	acctgcgcc	ggaacgcac	gaagccccgc	ccgaggaaac	cggcaaggac				840
gtccgcgtcg	tggccagacc	ggcgcgctcg	ttgtgggcgc	gcttctacga	cctcgacggc				900
caggtgccgc	tgttcgtcga	tcgcaacagc	cgtccggtgc	ccttcgcoga	gcttcccaac				960
gagcgtcgta	cggcgtatgg	ctggtatggc	acctggccgg	aaaagctgct	ggcacaggaa				1020
ctcccgcgct	ggcgcaaggt	ccatgcggcc	agcgcgggcg	ctccggcccc	ttga				1074

<210>	96
<211>	357
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

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<221> SIGNAL
<222> (1) ... (31)

<221> DOMAIN
<222> (32) ... (357)
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<223> Catalytic domain

<400> 96

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Met Thr Leu Pro Val Val Ser Leu Arg Val Leu Leu Ala Leu Leu Ala
 1          5          10          15
Thr Ser Pro Val Ala Cys Ala Gly Ala Ala Ala Pro Ala Thr Ala Thr
          20          25          30
Asp Pro Val Ala Glu Asn Met Leu Leu Leu Gln Thr Ala Ser Gly Gly
          35          40          45
Trp Ser Lys His Tyr Arg Glu Lys Lys Val Asp Tyr Ala Arg Asp Tyr
          50          55          60
Asp Ala Ala Glu Arg Ala Ala Leu Arg Ala Pro Asp Arg His Asp Asp
65          70          75          80
Ala Thr Ile Asp Asn Lys Ala Thr Thr Thr Glu Ile Ala Tyr Leu Val
          85          90          95
Gln Ala His Ala Arg Thr Gly Asn Pro Ala Tyr Leu Asp Gly Ala Arg
          100          105          110
Arg Gly Val Glu Tyr Leu Leu Arg Ala Gln Tyr Pro Asn Gly Gly Trp
          115          120          125
Pro Gln Phe Tyr Pro Asp His Ser Ser Tyr Arg His Gln Ile Thr Leu
          130          135          140
Asn Asp Asp Ala Met Val His Ala Ile Thr Val Leu Gln Asp Ile Ala
145          150          155          160
Ala Gly Arg Asn Gly Met Gln Val Leu Ala Pro Glu Phe Gly Val Arg
          165          170          175
Ala Ala Ala Ala Ala Gln Arg Gly Ile Gly Asn Leu Leu Glu Leu Gln
          180          185          190
Val Arg Ile Ala Gly Val Pro Thr Ile Trp Ala Ala Gln Tyr Asp Glu
          195          200          205
Thr Ser Leu Gln Pro Ala Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu
          210          215          220
Ala Val Ala Glu Ser Val Gly Val Val Arg Leu Leu Met Arg Gln Pro
225          230          235          240
Ala Pro Asp Ala Arg Thr Val Ala Ala Ile Glu Ala Ala Ala Asp Trp
          245          250          255
Leu Glu Ala His Arg Leu Pro Asp Leu Ala Leu Glu Arg Ile Glu Ala
          260          265          270
Pro Ala Glu Glu Thr Gly Lys Asp Val Arg Val Val Ala Arg Pro Gly
          275          280          285
Ala Ser Leu Trp Ala Arg Phe Tyr Asp Leu Glu Arg Gln Val Pro Leu
          290          295          300
Phe Val Asp Arg Asn Ser Arg Pro Val Pro Phe Ala Glu Leu Pro Asn
305          310          315          320
Glu Arg Arg Thr Gly Tyr Gly Trp Tyr Gly Thr Trp Pro Glu Lys Leu
          325          330          335
Leu Ala Gln Glu Leu Pro Arg Trp Arg Lys Val His Ala Ala Ser Ala
          340          345          350
Gly Ala Pro Ala Arg
          355

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<210> 97

<211> 2097

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 97

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cagcgcagcg	tcgatgcgat	cgtcgccgcg	gacggcaccg	gacagtttgc	gacggtgcag	180
gaggcgatca	acgccgcgcc	gcagaacacc	agcacgacca	gccgctggat	catcctcgtc	240
aaaccaggca	cgtatcgcga	ggtcgtctac	gtgcagcgctg	agaagcgctt	cgtcacgctg	300
atcggcgaag	acccggcacg	gacgacgac	acgtaccacc	tcaaagcgctc	tgacgtgggg	360
ctcgacggca	agcccacgcg	cacgtttcgc	acgccgacga	tggtggtgga	tgccgacgat	420
ttcacgatcg	agaacctcac	catcgagaac	ggggcagggc	cggtcgggtca	agcgctggcc	480
ttgcgagtgg	acggcgatcg	cgtgacgggtg	aggaacagcc	gcctgctggg	ctggcaggac	540
acgatctttc	tcaaccgtgg	gcgccactac	ttcgaggact	cgttcatcgg	cgggcacgtg	600
gatttcattt	tcggcgccgc	gacggcggtg	ttcgagcgat	gccatcttcg	cgctggcgcg	660
gacggctacc	tcacggccgc	gtccacgccc	gcggagcaac	gattcggctt	cgtgttctctg	720
aacagcatcg	tcagtggaga	agctggcgcc	cgcacgtacc	tcggtcgacc	gtggcgggcg	780
ttcgcgcacg	tggccttcat	caagacgacg	atgggcgagg	tggtgcgccc	ggtgggctgg	840
aacaactggg	accggccgga	gcgtgagaag	accgtgcgtt	ttctcgaagc	aggcaccagc	900
ggcgcggggc	gcagcgtcgc	tgcgcgcgtc	gcctggggcg	gcgtcgccac	gccagccgag	960
ctcgctgac	tgacgaccga	ggtggtgctt	ggcggcaccg	acggctggga	cccgcgtcgc	1020
gtcgccccgt	acccgtcggc	cgttcgcgcc	aacgcggcgc	cgctgccgcg	gccgcgggg	1080
cccagcgtcg	ctggcccgca	gagcccgcgc	gccttgacgt	gggaccagggt	cgcgcgccag	1140
ccagcgtcgt	ggctggccac	acccgaagcg	ctgcggattg	ccgagaacgt	gcgcctctat	1200
caacggcaca	ctggcggtcg	gcccataaac	ctcgacatgg	cgcagccgtt	gacggacgcc	1260
gatcgcgcg	gtctcacggc	cgatcgcgcg	ctcgacgact	cgaccatcga	caatggcgcc	1320
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caggcgtcga	tgctggctgg	gatcgactac	ctgctcgcg	cccagtatcc	aaacggcggc	1440
tggccgcagt	atttcccgt	ccgcaacgac	tactcgcgcc	acatcacgtt	caacgacgac	1500
gcgatgatcg	cggccgcgac	gatcctgcag	tcggtcgcg	tggcccgccc	gccgttcgcc	1560
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attctggcct	cgagattcgc	cgtcaacggc	cagctcactg	gctggtgcca	gcagcacgat	1680
gcacgcacgc	tggagccagc	gcgcggcgcg	acctacgagc	atccatcgat	cagtggccgc	1740
gaaaccgtga	cgatcgtcaa	tttcctgcgg	tcgatcgaac	cgcgcgaccg	ccagacccaa	1800
gccgccatcg	atgccgcgat	ggagtggctc	aaggccgtgc	agatccgcgg	ctggcgcacg	1860
gagcggcggc	ccgatccctc	aggaccgggc	ggttacgacg	tggtgatggt	ggaggacccc	1920
aacgcggcgc	cgctctgggc	ccgcttctac	gagattggca	ccaatcgccc	gatctactcg	1980
ggcggggacg	gcgtcatcaa	gtaccggctc	gccgagatcg	aaattgaacg	gcggaccggc	2040
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<210> 98
 <211> 698
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> DOMAIN
 <222> (45)...(333)
 <223> Pectin methyl esterase domain

<221> DOMAIN
 <222> (336)...(698)
 <223> Catalytic domain

<400> 98
 Met Asn Ala Ala Gly Ser Arg Arg Phe Ala Gln Leu Val Val Ala Asp
 1 5 10 15
 Leu Arg Arg Leu Val Pro Ala Leu Ala Pro Phe Phe Arg Asp Glu Pro
 20 25 30
 Leu Ala Gly Gly Val Ala Ala Leu Gln Arg Ser Val Asp Ala Ile Val
 35 40 45

Ala Ala Asp Gly Thr Gly Gln Phe Ala Thr Val Gln Glu Ala Ile Asn
 50 55 60
 Ala Ala Pro Gln Asn Thr Ser Thr Thr Ser Arg Trp Ile Ile Leu Val
 65 70 75 80
 Lys Pro Gly Thr Tyr Arg Glu Val Val Tyr Val Gln Arg Glu Lys Arg
 85 90 95
 Phe Val Thr Leu Ile Gly Glu Asp Pro Ala Arg Thr Thr Ile Thr Tyr
 100 105 110
 His Leu Lys Ala Ser Asp Val Gly Leu Asp Gly Lys Pro Ile Gly Thr
 115 120 125
 Phe Arg Thr Pro Thr Met Val Val Asp Ala Asp Asp Phe Thr Ile Glu
 130 135 140
 Asn Leu Thr Ile Glu Asn Gly Ala Gly Pro Val Gly Gln Ala Leu Ala
 145 150 155 160
 Leu Arg Val Asp Gly Asp Arg Val Thr Val Arg Asn Ser Arg Leu Leu
 165 170 175
 Gly Trp Gln Asp Thr Ile Phe Leu Asn Arg Gly Arg His Tyr Phe Glu
 180 185 190
 Asp Ser Phe Ile Gly Gly His Val Asp Phe Ile Phe Gly Gly Ala Thr
 195 200 205
 Ala Val Phe Glu Arg Cys His Leu Arg Ala Trp Arg Asp Gly Tyr Leu
 210 215 220
 Thr Ala Ala Ser Thr Pro Ala Glu Gln Arg Phe Gly Phe Val Phe Leu
 225 230 235 240
 Asn Ser Ile Val Ser Gly Glu Ala Gly Ala Arg Thr Tyr Leu Gly Arg
 245 250 255
 Pro Trp Arg Ala Phe Ala His Val Ala Phe Ile Lys Thr Thr Met Gly
 260 265 270
 Glu Val Val Arg Pro Val Gly Trp Asn Asn Trp Asp Arg Pro Glu Arg
 275 280 285
 Glu Lys Thr Val Arg Phe Leu Glu Ala Gly Thr Ser Gly Ala Gly Gly
 290 295 300
 Ser Val Ala Ala Arg Val Ala Trp Ala Arg Val Ala Thr Pro Ala Glu
 305 310 315 320
 Leu Ala Asp Leu Thr Thr Glu Val Val Leu Gly Gly Thr Asp Gly Trp
 325 330 335
 Asp Pro Arg Arg Val Ala Pro Tyr Pro Ser Ala Val Arg Ala Asn Ala
 340 345 350
 Ala Pro Leu Pro Arg Pro Pro Gly Pro Asp Val Ala Gly Pro Gln Ser
 355 360 365
 Pro Pro Ala Leu Thr Trp Asp Gln Val Ala Arg Gln Pro Ala Ser Trp
 370 375 380
 Leu Ala Thr Pro Glu Ala Leu Arg Ile Ala Glu Asn Val Arg Leu Tyr
 385 390 395 400
 Gln Arg His Thr Gly Trp Pro Lys Asn Leu Asp Met Ala Gln Pro
 405 410 415
 Leu Thr Asp Ala Asp Arg Ala Arg Leu Thr Ala Asp Arg Ala Leu Asp
 420 425 430
 Asp Ser Thr Ile Asp Asn Gly Ala Thr Thr Arg Gln Ile Glu Phe Leu
 435 440 445
 Ala Arg Ile Ala Ala Ala Asn Arg Asp Glu Arg Ala Gln Ala Ser Met
 450 455 460
 Leu Ala Gly Ile Asp Tyr Leu Leu Ala Ala Gln Tyr Pro Asn Gly Gly
 465 470 475 480
 Trp Pro Gln Tyr Phe Pro Leu Arg Asn Asp Tyr Ser Arg His Ile Thr
 485 490 495
 Phe Asn Asp Asp Ala Met Ile Ala Ala Ala Thr Ile Leu Gln Ser Val
 500 505 510
 Ala Leu Ala Arg Pro Pro Phe Ala Gly Val Asp Ala Thr Arg Arg Arg

515	520	525
Arg Ala Glu Ala Val	Ala Arg Ala His Arg	Val Ile Leu Ala Ser
530	535	540
Gln Ile Arg Val Asn Gly	Gln Leu Thr Gly Trp	Cys Gln Gln His Asp
545	550	555
Ala Arg Thr Leu Glu Pro	Ala Arg Gly Arg Thr	Tyr Glu His Pro Ser
565	570	575
Ile Ser Gly Arg Glu Thr	Val Thr Ile Val Asn Phe	Leu Arg Ser Ile
580	585	590
Glu Pro Arg Asp Arg Gln	Thr Gln Ala Ala Ile Asp	Ala Ala Met Glu
595	600	605
Trp Leu Lys Ala Val Gln	Ile Arg Gly Trp Arg Thr	Glu Arg Arg Pro
610	615	620
Asp Pro Ser Gly Pro Gly	Gly Tyr Asp Val Val Met	Val Glu Asp Pro
625	630	635
Asn Ala Ala Pro Leu Trp	Ala Arg Phe Tyr Glu Ile	Gly Thr Asn Arg
645	650	655
Pro Ile Tyr Ser Gly Arg	Asp Gly Val Ile Lys Tyr	Arg Leu Ala Glu
660	665	670
Ile Glu Ile Glu Arg Arg	Thr Gly Tyr Ser Trp Val	Gly Pro Tyr Ala
675	680	685
Gln Ala Leu Leu Asp Glu	Glu Arg Arg Lys	
690	695	

<210> 99

<211> 1782

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 99

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ttttcgacca	cggatggcgg	caatgtgtca	gggtcaaaat	cctttaccgc	ctcaagccac	180
acccaaatcc	agcaaactct	tgaggatgcc	aaagatggca	attatccggt	ggtgatcacc	240
tacaccggca	atgaggattc	actgattaac	caagtcgtcc	gggatcacac	cgtcgattct	300
tcaggcaact	gccctaaagc	gcgttggaa	gatgcctacc	gcaaagtcga	aatcaaagaa	360
atgaccaagg	gtgtcaccat	tcagggtgcc	aatggttcgt	cggcgaattt	cggaatcgtg	420
gtgaataaat	ccagcaacgt	gattattcgc	aacatgaaga	ttggtgcact	gggcggcgct	480
aataacgatg	cggatatgat	ccgtgtggac	agcgggtgtga	acgtctggat	cgatcacaa	540
gaattattcg	ccgtgaacaa	cgagtgtaa	ggttcaccgc	atggcgatct	gacctttgaa	600
agcgcgattg	atatcaaaaa	agcctcgcaa	gatatcaccg	tgtcctacaa	cgtgattcgc	660
gacagtaaaa	aagtcggttt	ggatggctcc	agcagcagcg	atatcgccgg	cggccgcaaa	720
attactttcc	accacaatat	ctaccgcaac	gtagggtgcg	gcttaccttt	gcagcgcggc	780
ggttgacgc	acatgtacaa	caacctgtac	gacggcatta	ccagctcggg	catcaacgtg	840
cgccaaaacg	ggtatgcgtt	aattgaaagc	aactgggttc	aaaacgcggt	taaccgggtc	900
acctgccgtt	ttgacagcag	caactgcggc	aagtgggatc	tgcgcaacaa	taacatccgc	960
aaccgcgggtg	attttgcgac	ttacaacatc	acctggacca	gtggcggcac	catcgacgcc	1020
accaactgga	ccaccactgc	gcccttcctt	atcagcattc	cctacagcta	ttcaccgggt	1080
actccgcaat	gtgtgaaaga	tcgtctggcg	agttacgcgg	gtgtgggtaa	aaacggcgcg	1140
cagctgactg	cctcggcctg	cgggtgtgcg	gcacgtccca	cacctgcac	gtccacacct	1200
gcaagttcca	gctctgcggc	aaacagttcc	gctgcacag	gcagtgtgag	tttgggtggc	1260
agtgccggta	atgcatcggg	tgcacttaac	tggaccgtga	atgccaacat	taatgcgtg	1320
gaaatttatc	aggatacggg	ttctgatccc	cgcggacgtg	tgcgcattgc	gtcgtgcca	1380
accagcgca	ccaactacac	cgcaacaggt	ctgagcaacg	gcactaccta	ttacttctgg	1440
gtgaaatata	gcaccaccaa	taatgtgtgg	agcaactcca	atgtgttcag	cgccaagcca	1500
agttcaggta	caaccccgctc	atcatccagc	agcgcggctt	catcaacgcc	aagtgggtgca	1560

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ccggtgttaa gtggtacagg tgattaccca agcggcttct ccaagtgtgc tgatctgggt 1620
ggcacctgct cagtcgcctc gggcgatggt tgggttgctt ttggtcgcaa aggcaagtgg 1680
gtcaccacaaa aagtgtcagt cggtagctct attgcctgta ccgttgccgc gtttggatct 1740
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<210> 100
 <211> 593
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(35)

<221> DOMAIN
 <222> (36)...(593)
 <223> Catalytic domain

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<400> 100
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Ser Leu Thr Ala Met Ala Ala Ala Val Ala Met Ile Ala Gly Thr Ser
      20             25             30
Ala Phe Ala Ala Ser Thr Gly Gly Phe Ser Thr Thr Asp Gly Gly Asn
      35             40             45
Val Ser Gly Ser Lys Ser Phe Thr Ala Ser Ser His Thr Gln Ile Gln
      50             55             60
Gln Ile Leu Glu Asp Ala Lys Asp Gly Asn Tyr Pro Val Val Ile Thr
      65             70             75             80
Tyr Thr Gly Asn Glu Asp Ser Leu Ile Asn Gln Val Val Arg Asp His
      85             90             95
Thr Val Asp Ser Ser Gly Asn Cys Pro Lys Ala Arg Trp Asn Asp Ala
      100            105            110
Tyr Arg Lys Val Glu Ile Lys Glu Met Thr Lys Gly Val Thr Ile Gln
      115            120            125
Gly Ala Asn Gly Ser Ser Ala Asn Phe Gly Ile Val Val Asn Lys Ser
      130            135            140
Ser Asn Val Ile Ile Arg Asn Met Lys Ile Gly Ala Leu Gly Gly Ala
      145            150            155            160
Asn Asn Asp Ala Asp Met Ile Arg Val Asp Ser Gly Val Asn Val Trp
      165            170            175
Ile Asp His Asn Glu Leu Phe Ala Val Asn Asn Glu Cys Lys Gly Ser
      180            185            190
Pro Asp Gly Asp Leu Thr Phe Glu Ser Ala Ile Asp Ile Lys Lys Ala
      195            200            205
Ser Gln Asp Ile Thr Val Ser Tyr Asn Val Ile Arg Asp Ser Lys Lys
      210            215            220
Val Gly Leu Asp Gly Ser Ser Ser Ser Asp Ile Ala Gly Gly Arg Lys
      225            230            235            240
Ile Thr Phe His His Asn Ile Tyr Arg Asn Val Gly Ala Arg Leu Pro
      245            250            255
Leu Gln Arg Gly Gly Trp Thr His Met Tyr Asn Asn Leu Tyr Asp Gly
      260            265            270
Ile Thr Ser Ser Gly Ile Asn Val Arg Gln Asn Gly Tyr Ala Leu Ile
      275            280            285
Glu Ser Asn Trp Phe Gln Asn Ala Val Asn Pro Val Thr Cys Arg Phe
      290            295            300

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Asp Ser Ser Asn Cys Gly Lys Trp Asp Leu Arg Asn Asn Asn Ile Arg
 305 310 315 320
 Asn Pro Gly Asp Phe Ala Thr Tyr Asn Ile Thr Trp Thr Ser Gly Gly
 325 330 335
 Thr Ile Asp Ala Thr Asn Trp Thr Thr Thr Ala Pro Phe Pro Ile Ser
 340 345 350
 Ile Pro Tyr Ser Tyr Ser Pro Val Thr Pro Gln Cys Val Lys Asp Arg
 355 360 365
 Leu Ala Ser Tyr Ala Gly Val Gly Lys Asn Gly Ala Gln Leu Thr Ala
 370 375 380
 Ser Ala Cys Gly Gly Ala Ala Ser Ser Thr Pro Ala Ser Ser Thr Pro
 385 390 395 400
 Ala Ser Ser Ser Ser Ala Ala Asn Ser Ser Ala Ala Ser Gly Ser Val
 405 410 415
 Ser Leu Gly Gly Ser Ala Gly Asn Ala Ser Val Ala Leu Asn Trp Thr
 420 425 430
 Val Asn Ala Asn Ile Asn Ala Leu Glu Ile Tyr Gln Asp Thr Asp Ser
 435 440 445
 Asp Pro Ala Gly Arg Val Arg Ile Ala Ser Leu Pro Thr Ser Ala Thr
 450 455 460
 Asn Tyr Thr Ala Thr Gly Leu Ser Asn Gly Thr Thr Tyr Tyr Phe Trp
 465 470 475 480
 Val Lys Tyr Arg Thr Thr Asn Asn Val Trp Ser Asn Ser Asn Val Phe
 485 490 495
 Ser Ala Lys Pro Ser Ser Gly Thr Thr Pro Ser Ser Ser Ser Ala
 500 505 510
 Ala Ser Ser Thr Pro Ser Gly Ala Pro Val Leu Ser Gly Thr Gly Asp
 515 520 525
 Tyr Pro Ser Gly Phe Ser Lys Cys Ala Asp Leu Gly Gly Thr Cys Ser
 530 535 540
 Val Ala Ser Gly Asp Gly Trp Val Ala Phe Gly Arg Lys Gly Lys Trp
 545 550 555 560
 Val Thr Lys Lys Val Ser Val Gly Ser Ser Ile Ala Cys Thr Val Ala
 565 570 575
 Ala Phe Gly Ser Asp Pro Gln Gly Asn Pro Asn Lys Cys Ser Tyr Lys
 580 585 590
 Lys

<210> 101
 <211> 1404
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 101
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 atcgaccgga gtgatgcgtt cggccaagct gatccatgga aaaccgtcta tccgcaaatac 120
 ctgcgtcgca tacggccacc gaaatttccg aagcgagatt tcatcatcac tagattcggc 180
 gcaaagccgg gaaccgacag cgccgctgcg atcgcaaaag ctatcaccgc gtgcagcaag 240
 gcaggcggag gacgtgttct cgttcccgcga ggagagtttc tcaccggagc gatccatctg 300
 aaatcgaacg taaactttca cgtgtcaaaa ggcgcgacgc tgaaattctc gaccgaccgc 360
 aaggcatatc tcccgattgt acatacgcga tgggaaggaa tggagctgat gcatctgtca 420
 ccgttcacatc acgcttatga gcagacgaac atcgctatca cgggtcaggg aacgctcgac 480
 ggccaggga aatcattctt ctggaaatgg catggcaatc cggcttatgg cggcgatccg 540
 aacacgctca gccaacggcc cgctcgtgcg cggctttacg agatgatgga taagaatgtg 600
 ccggtcgcgg aacgtgtctt cggctcgcga cattatctgc ggccgcagtt tattcagccg 660

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tacaaatgca ggaacgtttt gatcgaagat gtgacgatcg tcgattcgcc gatgtgggaa 720
gttcatccgg tgctttgcga gaacgtcacg gtccgaaatg ttcacatttc atcgcatggt 780
ccgaacaatg acggatgcga tccggagtcg tgcaaggacg tactgatcga caactgtttt 840
ttcgacaccg gcgacgattg catcgcgatc aagtccggcc gcaacaatga cggtcgtcgg 900
atcaatgtcc cgaccgagaa catcatcgtc cgcaactgca caatgaaaga cggtcatggc 960
ggcatcacgg tcggcagtga gatttcggga ggcgtgcgaa atctttttgc gcacgattgt 1020
cgactcgaca gtgcggatct ctggaccgag cttcgcgatc agaacaatgc gtcgcgaggc 1080
ggcaagctcg agaattttta ttttcggaat ataacggtcg gccagggtcg acgcgctgtg 1140
gtcgagatcg attttaatta cgaggaaggc gcgaaaggct cgtatattcc tgtcgttcga 1200
aattatgttg ttgaaggact gacatgcgcc acaggcaatc gcgccgtcga tctgcaagga 1260
ttggacaacg cgccgatcta caatgtaacg ctgcgaaact gtacgtttgg ttctgtccga 1320
aatcgtagtg ttgtgaaaaa cgttcgtgga cttcgggtcg agaatgtgaa gatcggcggc 1380
aggatcgtaa acgaactggg atga 1404

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<210> 102
 <211> 467
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(28)

<221> DOMAIN
 <222> (78)...(459)
 <223> Catalytic domain

<400> 102

Met	Thr	Ile	Asp	Arg	Arg	Glu	Phe	Leu	Ile	Asp	Leu	Ile	Ile	Gly	Thr
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Ala	Gly	Phe	Ala	Ile	Ala	Pro	Ser	Asp	Ala	Phe	Gly	Gln	Ala	Asp	Pro
			20					25					30		
Trp	Lys	Thr	Val	Tyr	Pro	Gln	Ile	Leu	Ala	Arg	Ile	Arg	Pro	Pro	Lys
		35					40					45			
Phe	Pro	Lys	Arg	Asp	Phe	Ile	Ile	Thr	Arg	Phe	Gly	Ala	Lys	Pro	Gly
	50					55					60				
Thr	Asp	Ser	Ala	Ala	Ala	Ile	Ala	Lys	Ala	Ile	Thr	Ala	Cys	Ser	Lys
	65				70					75				80	
Ala	Gly	Gly	Gly	Arg	Val	Leu	Val	Pro	Ala	Gly	Glu	Phe	Leu	Thr	Gly
			85					90						95	
Ala	Ile	His	Leu	Lys	Ser	Asn	Val	Asn	Phe	His	Val	Ser	Lys	Gly	Ala
			100					105					110		
Thr	Leu	Lys	Phe	Ser	Thr	Asp	Pro	Lys	Ala	Tyr	Leu	Pro	Ile	Val	His
		115					120					125			
Thr	Arg	Trp	Glu	Gly	Met	Glu	Leu	Met	His	Leu	Ser	Pro	Phe	Ile	Tyr
	130					135					140				
Ala	Tyr	Glu	Gln	Thr	Asn	Ile	Ala	Ile	Thr	Gly	Gln	Gly	Thr	Leu	Asp
	145				150					155				160	
Gly	Gln	Gly	Lys	Ser	Phe	Phe	Trp	Lys	Trp	His	Gly	Asn	Pro	Ala	Tyr
			165						170					175	
Gly	Gly	Asp	Pro	Asn	Thr	Leu	Ser	Gln	Arg	Pro	Ala	Arg	Ala	Arg	Leu
			180					185					190		
Tyr	Glu	Met	Met	Asp	Lys	Asn	Val	Pro	Val	Ala	Glu	Arg	Val	Phe	Gly
		195					200					205			
Leu	Gly	His	Tyr	Leu	Arg	Pro	Gln	Phe	Ile	Gln	Pro	Tyr	Lys	Cys	Arg
	210					215					220				
Asn	Val	Leu	Ile	Glu	Asp	Val	Thr	Ile	Val	Asp	Ser	Pro	Met	Trp	Glu

225					230				235				240				
Val	His	Pro	Val	Leu	Cys	Glu	Asn	Val	Thr	Val	Arg	Asn	Val	His	Ile		
				245					250					255			
Ser	Ser	His	Gly	Pro	Asn	Asn	Asp	Gly	Cys	Asp	Pro	Glu	Ser	Cys	Lys		
				260					265					270			
Asp	Val	Leu	Ile	Asp	Asn	Cys	Phe	Asp	Thr	Gly	Asp	Asp	Cys	Ile			
				275					280					285			
Ala	Ile	Lys	Ser	Gly	Arg	Asn	Asn	Asp	Gly	Arg	Arg	Ile	Asn	Val	Pro		
				290					295					300			
Thr	Glu	Asn	Ile	Ile	Val	Arg	Asn	Cys	Thr	Met	Lys	Asp	Gly	His	Gly		
305					310					315					320		
Gly	Ile	Thr	Val	Gly	Ser	Glu	Ile	Ser	Gly	Gly	Val	Arg	Asn	Leu	Phe		
				325					330					335			
Ala	His	Asp	Cys	Arg	Leu	Asp	Ser	Ala	Asp	Leu	Trp	Thr	Ala	Leu	Arg		
				340					345					350			
Val	Lys	Asn	Asn	Ala	Ser	Arg	Gly	Gly	Lys	Leu	Glu	Asn	Phe	Tyr	Phe		
				355					360					365			
Arg	Asn	Ile	Thr	Val	Gly	Gln	Val	Ala	Arg	Ala	Val	Val	Glu	Ile	Asp		
				370					375					380			
Phe	Asn	Tyr	Glu	Glu	Gly	Ala	Lys	Gly	Ser	Tyr	Ile	Pro	Val	Val	Arg		
385					390					395					400		
Asn	Tyr	Val	Val	Glu	Gly	Leu	Thr	Cys	Ala	Thr	Gly	Asn	Arg	Ala	Val		
				405					410					415			
Asp	Leu	Gln	Gly	Leu	Asp	Asn	Ala	Pro	Ile	Tyr	Asn	Val	Thr	Leu	Arg		
				420					425					430			
Asn	Cys	Thr	Phe	Gly	Ser	Val	Arg	Asn	Arg	Ser	Val	Val	Lys	Asn	Val		
				435					440					445			
Arg	Gly	Leu	Arg	Leu	Glu	Asn	Val	Lys	Ile	Gly	Gly	Arg	Ile	Val	Asn		
				450					455					460			
Glu	Leu	Val															
465																	

<210>	103
<211>	1101
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

[illegible]

aggccgccga agcggccctg a

1101

<210> 104

<211> 366

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(26)

<221> DOMAIN

<222> (27)...(366)

<223> Catalytic domain

<400> 104

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Met Asn Thr Ala Leu His Arg Val Ile Arg Leu Pro Leu Leu Leu Ala
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Leu Cys Leu Pro Ala Leu Gln Ala Gln Ala Thr Gln Thr Glu Pro Val
           20           25           30
Ala Glu Asn Met Leu Leu Leu Gln Thr Ala Ser Gly Gly Trp Ser Lys
           35           40           45
His His Gln Gly Lys Ala Val Asp Tyr Gly His Thr Phe Thr Asp Ala
 50           55           60
Glu Arg Ala Ala Leu Arg Ala Pro Asp Arg Arg Asp Asp Ala Thr Ile
65           70           75           80
Asp Asn Lys Ala Thr Thr Leu Glu Ile Val Ala Leu Leu Glu Ala His
           85           90           95
Gln Arg Thr Gly Asn Ala Ala Tyr Leu Ala Ala Ala Gln Arg Gly Val
           100          105          110
Asp Tyr Leu Leu Ala Ala Gln Tyr Pro Asn Gly Gly Trp Pro Gln Tyr
           115          120          125
Tyr Pro Asp Arg Ser Leu Tyr Arg His Gln Val Thr Phe Asn Asp Asp
           130          135          140
Ala Met Thr Arg Val Leu Glu Leu Leu Gln Asp Ile Val Glu Gly Lys
           145          150          155          160
Gly Ala Leu Ala Gln Leu Thr Pro Thr His Gly Glu Arg Ala Arg Ala
           165          170          175
Ala Leu Asp Arg Gly Ile Ala Cys Val Leu Ala Thr Gln Val Arg Ile
           180          185          190
Asp Gly Glu Leu Thr Leu Trp Ala Ala Gln Tyr Asp Glu Ala Thr Leu
           195          200          205
Gln Pro Ala Lys Ala Arg Ser Tyr Glu Leu Pro Ser Leu Ala Val Ala
           210          215          220
Glu Ser Val Gly Val Met Arg Leu Leu Met Arg Gln Pro Gln Pro Ser
           225          230          235          240
Pro Gln Val Leu Thr Ala Val Glu Ala Gly Ala Arg Trp Leu Glu Ala
           245          250          255
His Arg Met Arg Asp Leu Ala Arg Arg Lys Ile Asp Ala Pro Gly Glu
           260          265          270
Glu Thr Gly Gln Asp Val Val Ile Val Ala Glu Pro Gly Ala Ser Leu
           275          280          285
Trp Ala Arg Phe Tyr Asp Leu Gln His Gln Gln Pro Met Phe Val Asn
           290          295          300
Arg Glu Gly Glu Gln Val Ala Arg Phe Ala Asp Met Pro Asn Glu Arg
           305          310          315          320
Arg Val Gly Tyr Ala Trp Tyr Gly Val Trp Pro Glu Lys Leu Leu Gln

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325 330 335
 Gln Glu Leu Pro Arg Trp Tyr Asn Thr His Ala Glu Ala Leu Arg Ala
 340 345 350
 Ile Thr Pro Ala His Ala Glu Pro Arg Pro Pro Lys Arg Pro
 355 360 365

<210> 105
 <211> 1203
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 105
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 ggcgacaggc gctttccgcg ggatcatgcc gccgtttgcg cgggccttgc cctcgccgtg 120
 tcgtcggccg agccgggtccg ggcgcagggc gcggatgcgg atgcggatgg cccactgccc 180
 aggtggaaca ggaggctggt ggatcgcccc gaggactggt tcgcctccga cgagggacag 240
 cgcggttgccg ccaacgtcct ccgctaccaa tcggcggaag gagcctggcc caaaaacacc 300
 aatctggccg ccaactcccct tcgccccgag gacattccct cctcgacctc cggggtggcc 360
 aacacgatcg acaatgaagc caccaccgtg cccattcggg ttttgcccg tttcgcgcaa 420
 atcaacgagg acacggccag ccgcgaggcg gtccagcgcg gattggacta tctcctcaag 480
 gcgcaatata cgaacgggtg ctggccgcag tatttcccgc tccgccgcgg ctaccactcg 540
 cacatcacct acaacgacga cgccatggtg aatgtgctcg acctgctgct ggacgtgtcg 600
 ctgggcgagg agccgttcca ttttgtggac gaggatcgcc gccagcgggc cgcgaccgcc 660
 gtggagcggg ggatcgaatg catcctccgc acccaaattc ggaggaggga ccaaccacc 720
 ggctggtgcg cgcagtatga ccccgaaacc ttggccccgg cgtggggacg ggcgtacgag 780
 ccgcgctcga tttccggagc cgagaccgtc ggcgtggcgc ggtttctgat gcggctggag 840
 tcgccatcgc cggaagccgt cgaagccatc gaggggcgca tcgcctggct cgacacggtg 900
 ggcacgcagg aattgcgtct cgaatggttc accaacagcg agggcaagcg tgaccggcgc 960
 gtggtcgagg acgcttccgt gggcaccctt tgggcgcgct tttacgaact cgaaacgaac 1020
 cgcccccttg tcgtggaccg cgacgggggtg ctccgctacg acttcgcgga actgacggcg 1080
 gagcgccgcc aaggttacag ctactacggc acttggccgg cgccattgct ggccacggaa 1140
 tatccgcgct ggcgcaggat gaacgagtc gccctgctcg agtcgtcctt catctcgcat 1200
 tga 1203

<210> 106
 <211> 400
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(43)

<221> DOMAIN
 <222> (44)...(400)
 <223> Catalytic domain

<400> 106
 Met Gln Phe Ile Glu Thr Gln Gln Leu Gly Thr Ala Ala Lys Pro Val
 1 5 10 15
 Ala Gly Arg Gly Asp Arg Arg Phe Pro Arg Val Met Pro Ala Val
 20 25 30
 Cys Ala Gly Leu Ala Leu Ala Val Ser Ser Ala Glu Pro Val Arg Ala
 35 40 45

Gln	Gly	Ala	Asp	Ala	Asp	Ala	Asp	Gly	Pro	Leu	Pro	Arg	Trp	Asn	Arg
50					55						60				
Arg	Leu	Val	Asp	Arg	Pro	Glu	Asp	Trp	Phe	Ala	Ser	Asp	Glu	Gly	Gln
65					70					75					80
Arg	Val	Ala	Ala	Asn	Val	Leu	Arg	Tyr	Gln	Ser	Ala	Glu	Gly	Ala	Trp
				85					90					95	
Pro	Lys	Asn	Thr	Asn	Leu	Ala	Ala	Thr	Pro	Leu	Arg	Pro	Glu	Asp	Ile
			100					105					110		
Pro	Ser	Ser	Thr	Ser	Gly	Val	Ala	Asn	Thr	Ile	Asp	Asn	Glu	Ala	Thr
	115					120						125			
Thr	Val	Pro	Ile	Arg	Phe	Leu	Ala	Arg	Phe	Ala	Gln	Ile	Asn	Glu	Asp
130						135					140				
Thr	Ala	Ser	Arg	Glu	Ala	Val	Gln	Arg	Gly	Leu	Asp	Tyr	Leu	Leu	Lys
145					150					155					160
Ala	Gln	Tyr	Pro	Asn	Gly	Gly	Trp	Pro	Gln	Tyr	Phe	Pro	Leu	Arg	Arg
				165					170					175	
Gly	Tyr	His	Ser	His	Ile	Thr	Tyr	Asn	Asp	Asp	Ala	Met	Val	Asn	Val
			180					185					190		
Leu	Asp	Leu	Leu	Leu	Asp	Val	Ser	Leu	Gly	Glu	Glu	Pro	Phe	Asp	Phe
	195					200						205			
Val	Asp	Glu	Asp	Arg	Arg	Gln	Arg	Ala	Ala	Thr	Ala	Val	Glu	Arg	Gly
	210					215					220				
Ile	Glu	Cys	Ile	Leu	Arg	Thr	Gln	Ile	Arg	Gln	Glu	Asp	Gln	Pro	Thr
225					230					235					240
Gly	Trp	Cys	Ala	Gln	Tyr	Asp	Pro	Glu	Thr	Leu	Ala	Pro	Ala	Trp	Gly
				245					250					255	
Arg	Ala	Tyr	Glu	Pro	Pro	Ser	Ile	Ser	Gly	Ala	Glu	Thr	Val	Gly	Val
			260					265					270		
Ala	Arg	Phe	Leu	Met	Arg	Leu	Glu	Ser	Pro	Ser	Pro	Glu	Ala	Val	Glu
	275						280					285			
Ala	Ile	Glu	Gly	Ala	Ile	Ala	Trp	Leu	Asp	Thr	Val	Gly	Ile	Glu	Glu
	290					295					300				
Leu	Arg	Leu	Glu	Trp	Phe	Thr	Asn	Ser	Glu	Gly	Lys	Arg	Asp	Arg	Arg
305					310					315					320
Val	Val	Glu	Asp	Ala	Ser	Val	Gly	Thr	Leu	Trp	Ala	Arg	Phe	Tyr	Glu
				325					330					335	
Leu	Glu	Thr	Asn	Arg	Pro	Leu	Phe	Val	Asp	Arg	Asp	Gly	Val	Leu	Arg
			340					345					350		
Tyr	Asp	Phe	Ala	Glu	Leu	Thr	Ala	Glu	Arg	Arg	Gln	Gly	Tyr	Ser	Tyr
	355					360						365			
Tyr	Gly	Thr	Trp	Pro	Ala	Pro	Leu	Leu	Ala	Thr	Glu	Tyr	Pro	Arg	Trp
	370					375					380				
Arg	Arg	Met	Asn	Glu	Ser	Ala	Leu	Leu	Glu	Ser	Ser	Phe	Ile	Ser	His
385					390					395					400

<210> 107

<211> 1074

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 107

atgacgctac	ccgttgtttc	cctgcgcgta	ctgctggcgc	tgctggccac	gtcgccggtc	60
gcctgcgcgg	gcgctgcggc	acccgcgact	gcgaccgatc	cggtcgccga	gaacatgctg	120
cttctgcaga	ccgcctccgg	cggttggtcc	aagcactacc	gcgagaagaa	ggtcgactac	180
gcgcgcgact	acgacgccgc	cgagcgcgcc	gcgctgcgcg	cgccccgaccg	gcatgacgat	240
gccacgatcg	acaacaaggc	cacgaccacc	gagatcgcat	acctggtgca	ggcacatgcc	300

```

aggacgggca atccggccta cctcgacggc ggcgcgcgcg gcgtcgagta cctgctgcgc 360
gcgcagtacc cgaacggcgg ctggccgcag ttctaccccg accattcgtc ctaccggcac 420
cagatcacgc tcaacgacga tgcgatggtg cacgccatca ccgtgctgca ggacatcgcc 480
gcggggccgca acggcatgca ggtgctggcg ccggagttcg gcgtccgcgc cgccgcggcc 540
gcgcagcgcg gcatcggaaa cctgctcgag ttgcaggtgc ggatcgacgg ggtgccgacg 600
atctggggcg cgcagtacga cgagaccacc ctgcaaccgg ccaaggcccg tgcgtacgag 660
ttgccctcgc tggccgtggc cgaatcgggtg ggcgtgatgc gcctgctgat gcgccagccg 720
gggcctgatg cgcgcacgat cgccgcgacg gaggcggcgg cggactggct ggaggcgcac 780
cgccctgccg acctcgccct ggaacgcacg gaagcccccg ccgaggaaac cggcaaggac 840
gtccgcgtcg tggccagacc gggcgcgtcg ttgtgggcgc gcttctacga cctcgagcgg 900
caggtgccgc tgttcgtcga tcgcaacagc cgcccggttc cattcgccga gcttcccaac 960
gagcgtcgta ccggctatgg ctggtatggc acctggccgg aaaagctgct ggcacaggaa 1020
ctcccgcgct ggcgcaaggt ccatgcggcc agcgcgggcg ctccggcccg ttga 1074

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<210> 108
 <211> 357
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(31)

<221> DOMAIN
 <222> (32)...(357)
 <223> Catalytic domain

<400> 108

Met	Thr	Leu	Pro	Val	Val	Ser	Leu	Arg	Val	Leu	Leu	Ala	Leu	Leu	Ala
1				5					10				15		
Thr	Ser	Pro	Val	Ala	Cys	Ala	Gly	Ala	Ala	Ala	Pro	Ala	Thr	Ala	Thr
			20					25				30			
Asp	Pro	Val	Ala	Glu	Asn	Met	Leu	Leu	Leu	Gln	Thr	Ala	Ser	Gly	Gly
		35					40					45			
Trp	Ser	Lys	His	Tyr	Arg	Glu	Lys	Lys	Val	Asp	Tyr	Ala	Arg	Asp	Tyr
	50					55					60				
Asp	Ala	Ala	Glu	Arg	Ala	Ala	Leu	Arg	Ala	Pro	Asp	Arg	His	Asp	Asp
65					70					75				80	
Ala	Thr	Ile	Asp	Asn	Lys	Ala	Thr	Thr	Thr	Glu	Ile	Ala	Tyr	Leu	Val
				85					90					95	
Gln	Ala	His	Ala	Arg	Thr	Gly	Asn	Pro	Ala	Tyr	Leu	Asp	Gly	Ala	Arg
			100					105					110		
Arg	Gly	Val	Glu	Tyr	Leu	Leu	Arg	Ala	Gln	Tyr	Pro	Asn	Gly	Gly	Trp
		115					120					125			
Pro	Gln	Phe	Tyr	Pro	Asp	His	Ser	Ser	Tyr	Arg	His	Gln	Ile	Thr	Leu
	130					135					140				
Asn	Asp	Asp	Ala	Met	Val	His	Ala	Ile	Thr	Val	Leu	Gln	Asp	Ile	Ala
145					150					155				160	
Ala	Gly	Arg	Asn	Gly	Met	Gln	Val	Leu	Ala	Pro	Glu	Phe	Gly	Val	Arg
			165						170					175	
Ala	Ala	Ala	Ala	Ala	Gln	Arg	Gly	Ile	Gly	Asn	Leu	Leu	Glu	Leu	Gln
			180					185					190		
Val	Arg	Ile	Asp	Gly	Val	Pro	Thr	Ile	Trp	Ala	Ala	Gln	Tyr	Asp	Glu
		195					200					205			
Thr	Thr	Leu	Gln	Pro	Ala	Lys	Ala	Arg	Ala	Tyr	Glu	Leu	Pro	Ser	Leu
	210					215					220				
Ala	Val	Ala	Glu	Ser	Val	Gly	Val	Met	Arg	Leu	Leu	Met	Arg	Gln	Pro

225		230		235		240									
Gly	Pro	Asp	Ala	Arg	Thr	Ile	Ala	Ala	Ile	Glu	Ala	Ala	Ala	Asp	Trp
				245					250					255	
Leu	Glu	Ala	His	Arg	Leu	Pro	Asp	Leu	Ala	Leu	Glu	Arg	Ile	Glu	Ala
			260					265					270		
Pro	Ala	Glu	Glu	Thr	Gly	Lys	Asp	Val	Arg	Val	Val	Ala	Arg	Pro	Gly
		275					280					285			
Ala	Ser	Leu	Trp	Ala	Arg	Phe	Tyr	Asp	Leu	Glu	Arg	Gln	Val	Pro	Leu
	290					295					300				
Phe	Val	Asp	Arg	Asn	Ser	Arg	Pro	Val	Pro	Phe	Ala	Glu	Leu	Pro	Asn
305				310						315					320
Glu	Arg	Arg	Thr	Gly	Tyr	Gly	Trp	Tyr	Gly	Thr	Trp	Pro	Glu	Lys	Leu
			325					330						335	
Leu	Ala	Gln	Glu	Leu	Pro	Arg	Trp	Arg	Lys	Val	His	Ala	Ala	Ser	Ala
		340						345					350		
Gly	Ala	Pro	Ala	Arg											
		355													

<210> 109

<211> 1422

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 109

atgacgacac	gacgcgaatt	catcaaaggc	tttctactta	ccggagcagc	cgtggccgctc	60
gctccgcggtt	tgcttgcggtt	cgccgcggag	gcaagtccgt	gggaaacgat	gatgccttcg	120
atcctcgcac	gcatcagacc	acctcgtttt	ccgaaacgca	ccttctatct	caatcgattc	180
ggcgccaagg	gtgatggagt	cacagactgc	accgcggctt	ttcatcgcgc	gatcgatgaa	240
tgcaccaaag	ccggcgggtg	gaaagtcgtc	gtgccggcgg	gcacttatct	caccggcgcg	300
attcatttga	agagcaacgt	caacctcgaa	gtctcggaag	gcgcgacgat	caagttcagt	360
caggaccgca	aactactcct	gcctgttgct	ttctcgcgtt	gggaagggtg	cgaagtcttc	420
aactactcgc	ctttcattta	cgcgttcgaa	cagcgaaaca	tcgcgatcac	cggcaaaggc	480
acgctcgacg	gacagagtga	ttcggaacac	tggtggccgt	ggaacggccg	tccgcagtac	540
ggatggaaaag	aagggatgaa	acagcagcgt	cccgatcgca	acgcgttggt	cacaatggcg	600
gagaaaggcg	tgccgggtgcg	cgagcgcata	tttggcgaag	gtcattatct	gaggccgcag	660
ttcatttcagc	cgtaccgctg	ccagaacgtg	ctgatccagg	gcgtgacgat	tccggaactcg	720
ccgatgtggg	agattcatcc	ggtgttggtg	cgtaacgtga	ctattcacga	cgtgcacatc	780
gatagtcatg	gaccaaaca	cgacggctgc	aatcccgaat	cgtgcagcga	cgtgttgatt	840
aaggatagct	acttcgatac	cggcgacgac	tgcatcgcga	tcaaatacgg	acgcaacgcc	900
gacgggcggc	ggcttaaagc	gccgactgag	aacatcatcg	ttcaaggatg	tcgcatgaaa	960
gacggccacg	gtggaatcac	ggtcggcgag	gagatctcgg	gcggcgtgcg	aaacctgttt	1020
gccgagaatt	gccggctcga	cagtccaaac	ctcgatcacg	ccctgcgcgt	gaagaacaat	1080
gccatgcgcg	gcggattact	cgagaacttc	cacttccgta	acatcgaaat	cgggcagggtg	1140
gcccattgccg	tgattacgat	cgacttcaac	tacgaagagg	gcgcgaaaag	gtcgttcacg	1200
ccggtcgttc	gcgattacac	ggtcgatcgt	ttgcgcagca	cgaagagcaa	gcacgcactc	1260
gacgtccagg	gtctgcccgg	cgcgcgggtc	atcaactcgc	gattgacgaa	ctgcacattc	1320
aacgatgtgc	agcaaccgaa	cattctcaag	aacgtcgaac	aatcaacctt	tgaaaacgtc	1380
acgattaacg	gaaagacgat	cacacaaaca	ggatccaaag	aa		1422

<210> 110

<211> 474

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(21)

<221> DOMAIN

<222> (28)...(308)

<223> Pectin methyl esterase domain

<221> DOMAIN

<222> (309)...(637)

<223> Catalytic domain

<400> 110

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Met Thr Thr Arg Arg Glu Phe Ile Lys Gly Phe Leu Leu Thr Gly Ala
 1          5          10          15
Ala Val Ala Val Ala Pro Arg Leu Leu Ala Phe Ala Ala Glu Ala Ser
          20          25          30
Pro Trp Glu Thr Met Met Pro Ser Ile Leu Ala Arg Ile Arg Pro Pro
          35          40          45
Arg Phe Pro Lys Arg Thr Phe Tyr Leu Asn Arg Phe Gly Ala Lys Gly
          50          55          60
Asp Gly Val Thr Asp Cys Thr Ala Ala Phe His Arg Ala Ile Asp Glu
65          70          75          80
Cys Thr Lys Ala Gly Gly Lys Val Val Val Pro Ala Gly Thr Tyr
          85          90          95
Leu Thr Gly Ala Ile His Leu Lys Ser Asn Val Asn Leu Glu Val Ser
          100          105          110
Glu Gly Ala Thr Ile Lys Phe Ser Gln Asp Pro Lys His Tyr Leu Pro
          115          120          125
Val Val Phe Ser Arg Trp Glu Gly Val Glu Val Phe Asn Tyr Ser Pro
          130          135          140
Phe Ile Tyr Ala Phe Glu Gln Arg Asn Ile Ala Ile Thr Gly Lys Gly
145          150          155          160
Thr Leu Asp Gly Gln Ser Asp Ser Glu His Trp Trp Pro Trp Asn Gly
          165          170          175
Arg Pro Gln Tyr Gly Trp Lys Glu Gly Met Lys Gln Gln Arg Pro Asp
          180          185          190
Arg Asn Ala Leu Phe Thr Met Ala Glu Lys Gly Val Pro Val Arg Glu
          195          200          205
Arg Ile Phe Gly Glu Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro
          210          215          220
Tyr Arg Cys Gln Asn Val Leu Ile Gln Gly Val Thr Ile Arg Asn Ser
225          230          235          240
Pro Met Trp Glu Ile His Pro Val Leu Cys Arg Asn Val Thr Ile His
          245          250          255
Asp Val His Ile Asp Ser His Gly Pro Asn Asn Asp Gly Cys Asn Pro
          260          265          270
Glu Ser Cys Ser Asp Val Leu Ile Lys Asp Ser Tyr Phe Asp Thr Gly
          275          280          285
Asp Asp Cys Ile Ala Ile Lys Ser Gly Arg Asn Ala Asp Gly Arg Arg
          290          295          300
Leu Lys Ala Pro Thr Glu Asn Ile Ile Val Gln Gly Cys Arg Met Lys
305          310          315          320
Asp Gly His Gly Gly Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val
          325          330          335
Arg Asn Leu Phe Ala Glu Asn Cys Arg Leu Asp Ser Pro Asn Leu Asp
          340          345          350
His Ala Leu Arg Val Lys Asn Asn Ala Met Arg Gly Gly Leu Leu Glu
          355          360          365

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Asn	Phe	His	Phe	Arg	Asn	Ile	Glu	Val	Gly	Gln	Val	Ala	His	Ala	Val
370						375					380				
Ile	Thr	Ile	Asp	Phe	Asn	Tyr	Glu	Glu	Gly	Ala	Lys	Gly	Ser	Phe	Thr
385					390					395					400
Pro	Val	Val	Arg	Asp	Tyr	Thr	Val	Asp	Arg	Leu	Arg	Ser	Thr	Lys	Ser
				405					410					415	
Lys	His	Ala	Leu	Asp	Val	Gln	Gly	Leu	Pro	Gly	Ala	Pro	Val	Ile	Asn
			420					425					430		
Leu	Arg	Leu	Thr	Asn	Cys	Thr	Phe	Asn	Asp	Val	Gln	Gln	Pro	Asn	Ile
		435					440					445			
Leu	Lys	Asn	Val	Glu	Gln	Ser	Thr	Phe	Glu	Asn	Val	Thr	Ile	Asn	Gly
	450				455						460				
Lys	Thr	Ile	Thr	Gln	Thr	Gly	Ser	Lys	Glu						
465					470										

<210> 111
 <211> 1440
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 111

atgcaaaatc	gtcgagaatt	tttacaactt	ttatttgccg	gtgccggtgc	cggacttggt	60
ttgccgcaga	tttctttcgg	gcagactaaa	caagccgacg	cctggacgac	cgagtatccg	120
aagatttttag	ccagaatcaa	accgccgaaa	tttcgcaaaa	aagattttcc	gatcaccaaa	180
tatggagccg	ttgcggacgg	gaaaaccctg	gcgaccgaaa	gcatcaaaaa	agccatcgaa	240
gcgtgcgcca	aatcggggcg	cgggcgcgtc	gtcgtgcccc	agggagaatt	tttgaccggc	300
gcgattcatt	tgaaatcaaa	cgtcaatctg	cacatcacga	aaggcgcgac	cgtcaaattt	360
tccaccaacc	cgaaagatta	tctgccgatc	gttcacacgc	gctgggaagg	gatggaattg	420
atgcataatt	cgcctttaat	ttatgcctac	gagcaaaacca	acatcgccgt	caccggcgag	480
ggaacgctcg	acgggcaggg	caaggctttt	ttctggaaat	ggcacggaaa	cccgcgctac	540
ggcggaaatc	cggatgtgat	cagccagcgt	ccggcgcgcg	cccggctgta	tgaaatgatg	600
gaaaaaggcg	tgctgtggc	ggagcggatt	ttcggcgaaa	ctcagtatct	tcgcccgcag	660
tttatccagc	cctataaatg	caaaaatgtt	ttgatcgaa	gcgttaaaat	catcgattcg	720
ccgatgtggg	aagttcaccc	cgttttgtgc	gaaaaacgtg	cgatccgaaa	acttcatatt	780
tctaccacag	gaccgaacaa	cgacgggtgc	gatccggaaa	gctgcaagga	cgttttgatc	840
gaagactgct	atttcgacac	cggcgacgat	tgcattgcca	tcaaggcggg	gcgcaatgaa	900
gacgggcgac	gcatcaatgt	tccgaccgaa	aacgtcgtcg	tgccggggtg	cgtgatgaag	960
gacggtcacg	gcggaatcac	catcggaagc	gagatttccg	gcggcgtgcg	aaatgttttc	1020
gcggaaaaca	accggctcga	cagcgcggat	ttgtggactg	cgctgagagt	gaaaaacaac	1080
gcttcgcgcg	gcggaaaact	ggagaatttt	tacttccgcg	atatcaccgt	cgggcaggtc	1140
tcgcgcgcgg	tcgtcgaaat	agattttaat	tacgaggaag	gcgctaaagg	aaaacacacg	1200
ccggtcgttc	gcaattacgt	ggtcgaaaaat	ctaacctgca	ataaaggcaa	tcgagcggtc	1260
gatctgcagg	gcttgacaa	cgccccgatt	tacgacatca	cgatgaaaaa	ctgtacgttt	1320
aacgtggtcg	aaaagccgag	cgtcgtgaaa	aacgtcaaag	gcgtcaaact	ggaaaacgtg	1380
aagattaacg	gcaaagtcgt	cgagagtctg	gaaaatgctg	caacgacggc	taaaaaataa	1440

<210> 112
 <211> 479
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<221> SIGNAL
 <222> (1)...(27)

<221> DOMAIN

<222> (82)...(461)

<223> Catalytic domain

<400> 112

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Met  Gln Asn Arg  Arg Glu  Phe Leu  Gln Leu  Leu Phe Ala Gly Ala Gly
 1          5          10          15
Ala Gly Leu Val Leu Pro Gln Ile Ser Phe Gly Gln Thr Lys Gln Ala
          20          25          30
Asp Ala Trp Thr Thr Glu Tyr Pro Lys Ile Leu Ala Arg Ile Lys Pro
          35          40          45
Pro Lys Phe Arg Lys Lys Asp Phe Pro Ile Thr Lys Tyr Gly Ala Val
          50          55          60
Ala Asp Gly Lys Thr Leu Ala Thr Glu Ser Ile Lys Lys Ala Ile Glu
65          70          75          80
Ala Cys Ala Lys Ser Gly Gly Gly Arg Val Val Val Pro Gln Gly Glu
          85          90          95
Phe Leu Thr Gly Ala Ile His Leu Lys Ser Asn Val Asn Leu His Ile
          100          105          110
Thr Lys Gly Ala Thr Val Lys Phe Ser Thr Asn Pro Lys Asp Tyr Leu
          115          120          125
Pro Ile Val His Thr Arg Trp Glu Gly Met Glu Leu Met His Ile Ser
130          135          140
Pro Leu Ile Tyr Ala Tyr Glu Gln Thr Asn Ile Ala Val Thr Gly Glu
145          150          155          160
Gly Thr Leu Asp Gly Gln Gly Lys Ala Phe Phe Trp Lys Trp His Gly
          165          170          175
Asn Pro Arg Tyr Gly Gly Asn Pro Asp Val Ile Ser Gln Arg Pro Ala
          180          185          190
Arg Ala Arg Leu Tyr Glu Met Met Glu Lys Gly Val Pro Val Ala Glu
          195          200          205
Arg Ile Phe Gly Glu Thr Gln Tyr Leu Arg Pro Gln Phe Ile Gln Pro
210          215          220
Tyr Lys Cys Lys Asn Val Leu Ile Glu Gly Val Lys Ile Ile Asp Ser
225          230          235          240
Pro Met Trp Glu Val His Pro Val Leu Cys Glu Asn Val Thr Ile Arg
          245          250          255
Lys Leu His Ile Ser Thr His Gly Pro Asn Asn Asp Gly Cys Asp Pro
          260          265          270
Glu Ser Cys Lys Asp Val Leu Ile Glu Asp Cys Tyr Phe Asp Thr Gly
          275          280          285
Asp Asp Cys Ile Ala Ile Lys Ala Gly Arg Asn Glu Asp Gly Arg Arg
290          295          300
Ile Asn Val Pro Thr Glu Asn Val Val Val Arg Gly Cys Val Met Lys
305          310          315          320
Asp Gly His Gly Gly Ile Thr Ile Gly Ser Glu Ile Ser Gly Gly Val
          325          330          335
Arg Asn Val Phe Ala Glu Asn Asn Arg Leu Asp Ser Ala Asp Leu Trp
          340          345          350
Thr Ala Leu Arg Val Lys Asn Asn Ala Ser Arg Gly Gly Lys Leu Glu
          355          360          365
Asn Phe Tyr Phe Arg Asp Ile Thr Val Gly Gln Val Ser Arg Ala Val
          370          375          380
Val Glu Ile Asp Phe Asn Tyr Glu Glu Gly Ala Lys Gly Lys His Thr
385          390          395          400
Pro Val Val Arg Asn Tyr Val Val Glu Asn Leu Thr Cys Asn Lys Gly
          405          410          415
Asn Arg Ala Val Asp Leu Gln Gly Leu Asp Asn Ala Pro Ile Tyr Asp

```

			420				425				430					
Ile	Thr	Met	Lys	Asn	Cys	Thr	Phe	Asn	Val	Val	Glu	Lys	Pro	Ser	Val	
			435				440				445					
Val	Lys	Asn	Val	Lys	Gly	Val	Lys	Leu	Glu	Asn	Val	Lys	Ile	Asn	Gly	
			450				455				460					
Lys	Val	Val	Glu	Ser	Leu	Glu	Asn	Ala	Ala	Thr	Thr	Ala	Lys	Lys		
			465				470				475					

<210>	113
<211>	1017
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample

<400>	113									
atgaagatat	ttttaacaat	attgctctcg	gcattattca	gcattttcaa	tgcacaggtg					60
ctatcggatc	ctgttgcgga	tcgtatgacc	agctaccaac	ttaaaaacgg	aggctggccg					120
aagcacttgg	ccgataaatc	tggttgtaac	tattcaaaac	ctctctcacc	tgctttgcaa					180
aaagtcatcg	atcaatcgac	cgaaaagtct	gcgacaattg	ataataatgc	aaccacacgt					240
gagataaacc	atcttctcct	cgcttattcc	aaaaccaaca	atgacaagta	tcttcaagcg					300
gcgacaaaag	gtgttgagta	tatcctgagt	gctcaaaatg	acaaggagg	atggcctcaa					360
tattatctcg	acagtagctc	atatcgtgg	catatcacct	acaatgacgg	cgcgatgatt					420
aatgtattgg	aaattttact	ttccatatca	acaaaacaag	agccctatgc	tgttctaacg					480
aataaattta	acgaaagaat	agaaagggcc	ttaacacgag	ggattcactg	catcttacia					540
acccagggtta	aacaaggaga	taaactaacc	atctggggcg	cacagtacga	tcagaaaaca					600
atggaacctg	ctcaagccag	actgtttgaa	ccggtagcgt	tagcgacagc	ggaatcggcg					660
ggcattctcc	gctttttaat	gcgtcttgac	catcctactc	ccgaaataaa	aatgcaatc					720
aaccacgctg	tagaatggtt	ttcctcccat	aaagaggtag	gctatgatta	cgttaaaacg					780
gaaaaaaaacg	gaaaactttt	gcgggatttg	gtttcttcgc	cggcctctac	cgtatgggca					840
agatttttatg	acatcaggac	gaatcaacc	atctttgggt	atcgcgataa	tacgataaag					900
tattcgtctga	atgaaataag	cagggaacga	caaaatggct	actcttggtta	tggttaactgg					960
ccagaaaaqa	taattacaaa	agaatatgaa	aatggctta	agaaggtaaa	tgaataa					1017

<210>	114
<211>	338
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

```
<221> SIGNAL
<222> (1)...(18)
```

```
<221> DOMAIN
<222> (19)...(388)
<223> Catalytic domain
```

<400> 114															
Met	Lys	Ile	Phe	Leu	Thr	Ile	Leu	Leu	Ser	Ala	Leu	Phe	Ser	Ile	Ser
1				5					10					15	
Asn	Ala	Gln	Val	Leu	Ser	Asp	Pro	Val	Ala	Asp	Arg	Met	Thr	Ser	Tyr
			20					25					30		
Gln	Leu	Lys	Asn	Gly	Gly	Trp	Pro	Lys	His	Leu	Ala	Asp	Lys	Ser	Val
		35					40					45			
Val	Asn	Tyr	Ser	Lys	Pro	Leu	Ser	Pro	Ala	Leu	Gln	Lys	Val	Ile	Asp
	50					55				60					

Gln Ser Thr Glu Lys Ser Ala Thr Ile Asp Asn Asn Ala Thr Thr Arg
 65 70 75 80
 Glu Ile Asn His Leu Leu Leu Ala Tyr Ser Lys Thr Asn Asn Asp Lys
 85 90 95
 Tyr Leu Gln Ala Ala Thr Lys Gly Val Glu Tyr Ile Leu Ser Ala Gln
 100 105 110
 Asn Asp Lys Gly Gly Trp Pro Gln Tyr Tyr Pro Asp Ser Ser Tyr
 115 120 125
 Arg Gly Gln Ile Thr Tyr Asn Asp Gly Ala Met Ile Asn Val Leu Glu
 130 135 140
 Ile Leu Leu Ser Ile Ser Thr Lys Gln Glu Pro Tyr Ala Val Leu Thr
 145 150 155 160
 Asn Lys Phe Asn Glu Arg Ile Glu Arg Ala Leu Thr Arg Gly Ile His
 165 170 175
 Cys Ile Leu Gln Thr Gln Val Lys Gln Gly Asp Lys Leu Thr Ile Trp
 180 185 190
 Ala Ala Gln Tyr Asp Gln Lys Thr Met Glu Pro Ala Gln Ala Arg Leu
 195 200 205
 Phe Glu Pro Val Ala Leu Ala Thr Ala Glu Ser Ala Gly Ile Leu Arg
 210 215 220
 Phe Leu Met Arg Leu Asp His Pro Thr Pro Glu Ile Lys Asn Ala Ile
 225 230 235 240
 Asn His Ala Val Glu Trp Phe Ser Ser His Lys Glu Val Gly Tyr Asp
 245 250 255
 Tyr Val Lys Thr Glu Lys Asn Gly Lys Leu Leu Arg Asp Leu Val Ser
 260 265 270
 Ser Pro Ala Ser Thr Val Trp Ala Arg Phe Tyr Asp Ile Arg Thr Asn
 275 280 285
 Gln Pro Ile Phe Gly Asp Arg Asp Asn Thr Ile Lys Tyr Ser Leu Asn
 290 295 300
 Glu Ile Ser Glu Glu Arg Gln Asn Gly Tyr Ser Trp Tyr Gly Asn Trp
 305 310 315 320
 Pro Glu Lys Ile Ile Thr Lys Glu Tyr Glu Lys Trp Leu Lys Lys Val
 325 330 335
 Asn Glu

<210> 115
 <211> 996
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 115
 gtggccaagg cgatcggcgg tccgttgccg ccggcaccag ggcagggatc gccggtaacg 60
 tgggcgacga ttctccggca gccatcgccg tggtagcggt ccgcggacgc gaaggcggtt 120
 gccgaaaccg tgcgcgcgag ccagagagcc accggcggct ggccgaagaa cacggattgg 180
 acggcgctcc agagcgacgc tgagcggcag gcgctgcgaa atgcccgcg cgagaccgat 240
 tcgacgatcg acaatggcgc cacggtcacc gagcttcgct ttctcaccgg cgtgtatgtc 300
 gccacgcgcg acgagctttt acgggaggcc gtgcttcgcg gcctcgacta cctgctggcg 360
 tcgcagtaca gcaacggcgg ctggccacaa tactttccgt tgcggaccga ttactcgcgg 420
 gacatcacgt tcaacgacga cgcgatgacc ggctggtgac tgctgctgaa ggatgccgcg 480
 gacgggtcag caggtttcga attcgtcgac aaggcgagac gtgaccgcgc tgccgcggcc 540
 gtgacgcgcg ccacgcgggt gatcctccgc acgcagattc gggtaaacgg tacgctgacc 600
 ggctggtgcc agcagtacga cgccgacgcg ctgacgccgg cgcgcgggcg ctcgtacgag 660
 catccgtcga ttgcgagccg cgagacggtc gggatcgcg ggctgctgat gggcggtgccg 720
 aatccgtcgc cagagatcgt ggctgccgtt gacgcggctg ccgcatggtt gggtaaatcg 780

gaactgaagg	gtgtgcccg	ggcgacggcg	ccaggacttt	gggcgcgctt	ctacgacatc	840
gctacgaatc	ggccgatcta	ttcggggccgc	gacggcgctca	tcaagtaccg	gctcgacgag	900
atcgagctcg	agcggcgcac	aggctacagc	tgggttggcc	cgtagccgcg	ggcattttctg	960
acgaccgaat	atccgaaatg	gcggggcgga	cgatga			996

<210>	116
<211>	331
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample

```
<221> DOMAIN
<222> (1)...(331)
<223> Catalytic domain
```

<400>	116														
Met 1	Ala	Lys	Ala	Ile 5	Gly	Gly	Pro	Leu	Pro 10	Pro	Ala	Pro	Gly 15	Gln	Gly
Ser	Pro	Val	Thr 20	Trp	Ala	Thr	Ile	Leu 25	Arg	Gln	Pro	Ser	Pro 30	Trp	Tyr
Ala	Ser	Ala 35	Asp	Ala	Lys	Ala	Val 40	Ala	Glu	Thr	Val	Arg 45	Ala	Ser	Gln
Arg	Ala 50	Thr	Gly	Gly	Trp	Pro 55	Lys	Asn	Thr	Asp	Trp 60	Thr	Ala	Leu	Gln
Ser 65	Asp	Ala	Glu	Arg	Gln 70	Ala	Leu	Arg	Asn	Ala 75	Arg	Ala	Glu	Thr	Asp 80
Ser	Thr	Ile	Asp	Asn 85	Gly	Ala	Thr	Val	Thr 90	Glu	Leu	Arg	Phe	Leu 95	Thr
Arg	Val	Tyr	Val 100	Ala	Thr	Arg	Asp	Glu 105	Leu	Leu	Arg	Glu	Ala 110	Val	Leu
Arg	Gly	Leu	Asp 115	Tyr	Leu	Leu	Ala	Ser	Gln	Tyr	Ser	Asn 125	Gly	Gly	Trp
Pro	Gln 130	Tyr	Phe	Pro	Leu	Arg 135	Thr	Asp	Tyr	Ser	Arg 140	Asp	Ile	Thr	Phe
Asn 145	Asp	Asp	Ala	Met	Thr 150	Gly	Val	Val	Leu	Leu 155	Lys	Asp	Ala	Ala	Ala 160
Asp	Gly	Ser	Ala	Gly 165	Phe	Glu	Phe	Val	Asp 170	Lys	Ala	Arg	Arg	Asp 175	Arg
Ala	Ala	Ala	Ala 180	Val	Thr	Arg	Ala	Ile 185	Ala	Val	Ile	Leu	Arg 190	Thr	Gln
Ile	Arg	Val 195	Asn	Gly	Thr	Leu	Thr 200	Gly	Trp	Cys	Gln	Gln 205	Tyr	Asp	Ala
Asp	Ala 210	Leu	Thr	Pro	Ala	Arg 215	Gly	Arg	Ser	Tyr	Glu 220	His	Pro	Ser	Ile
Ala 225	Ser	Arg	Glu	Thr	Val	Gly 230	Ile	Ala	Arg	Leu 235	Leu	Met	Gly	Val	Pro 240
Asn	Pro	Ser	Pro	Glu 245	Ile	Val	Ala	Ala	Val 250	Asp	Ala	Ala	Ala	Ala 255	Trp
Leu	Gly	Lys	Ser 260	Glu	Leu	Lys	Gly	Val 265	Pro	Glu	Ala	Thr	Ala 270	Pro	Gly
Leu	Trp	Ala 275	Arg	Phe	Tyr	Asp	Ile 280	Ala	Thr	Asn	Arg	Pro 285	Ile	Tyr	Ser
Gly	Arg 290	Asp	Gly	Val	Ile	Lys 295	Tyr	Arg	Leu	Asp	Glu 300	Ile	Glu	Leu	Glu
Arg 305	Arg	Thr	Gly	Tyr	Ser	Trp 310	Val	Gly	Pro	Tyr	Ala 315	Ala	Ala	Phe	Leu 320
Thr	Thr	Glu	Tyr	Pro	Lys	Trp	Arg	Ala	Ala	Arg					

325

330

<210> 117
 <211> 1725
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

```

<400> 117
atgaagaatt ttggggtttg taactacaag ttttttgtag cggcaatgtc tgtcgcgtct      60
ttttcgtatg cggcaagcta tacaccccg tcaacagcag tttcgaaaat caacagctat      120
cgaggctatt cggagctgac ttcagctgca tccggcatgg atatcgacca gtacacctac      180
aacatgacca cttggcaaat cgcaaacggc ggtttttaca aagccatggc cgacaagtat      240
aaaagcgcgt atggcggcgg tcaaaaatcc gaatggcaag ctaaaggcgg tggcgacctc      300
ggcactatag acaacaacgc caccatccag gaaatgcgtt tgctcgccgt gcgttacaaa      360
gaaacgacga acaacaatta caaatccgca tttaagacaa gtttcaacaa ggcggtcaat      420
tttcttttga ccatgcagcg ctccaaaggc ggactcccac aagtttgccc caaacgcggc      480
aactattctg accaaatcac gctaaatgac aacgccatga tccgcgccat ggtcacgatg      540
atggatatcg ccaacaagac gagtccattt gattcggata tcatcgacga cgccacccgc      600
agcaaaatga aatcggctct cgacaaagcg gtcgattact tgctcaaggc gcaaactcgtg      660
aacgacggaa aggtcacggg atggtgcgcc cagcacgaca ccaacagcct cgccccgta      720
ggcgcacgag cctacgaact cccgagcaaa tccggcaacg aatccatggg cgttgtgtgg      780
tttttgatga actggccaga ccaaaacgaa gcaatccaga aggcggtcaa aggcgcaatc      840
gcttggtaca aaaagaataa actaaaagac aaggcggtta gcaagaccgc aggcgttgtg      900
gacaaggcgg gttcatcgct gtggttccgc ttttacgaag tcaacaacga caactacttt      960
ttctgcgacc gcgatggtgc tagcaccaag acgcaggact tcatgaaaat cagcgaagaa      1020
cgtcgcaagg gctaccagtg ggcaggcgat tacggctctg caattctagg caccgaaaat      1080
gcataccttg aagcactcgc caagatggac gacaactatg ttccacctcc gccagcacca      1140
gctatgtgcg gaaacgacac ttgcaaaacg tacatcgatg gcgttgactt tattgacatt      1200
caaggcggtca aggaacaac caacacggga ttcggttgcg aaggttacgc caacgttgac      1260
aactccaccg gaagctatgt gacctacggc gtcaccgat tcaaggaagg caaatacact      1320
ttgttcatca gctttgcaaa cggcgggtgt tccgcacgcg gttacagcgt ttctgcagga      1380
gacaagacgt tacttgaga cggcagcatg gaatctacag ccgcatggac cacttggaag      1440
atgcaatcca tcgaaatcga attgccaatg ggctatagcg aactcaagtt cacaagcctt      1500
tcgaaagacg gtatggcgaa catcgattac atcggctgga tgaacgatga tttgaaagtt      1560
ggcgaagttg aagtaccacg ctcatccatt gaagcaatac gcgccatccg caaagcccag      1620
caggacaacc gctactttgt ggactttggc ggcaacaata atagcgcagg ggcttacttt      1680
aagcgtggca tcaacacggt ccgcgtgaat ggaagatga ggtaa      1725

```

<210> 118
 <211> 574
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(24)

<221> DOMAIN
 <222> (25)...(574)
 <223> Catalytic domain

```

<400> 118
Met Lys Asn Phe Gly Phe Gly Asn Tyr Lys Phe Phe Val Ala Ala Met
  1                      5                      10                      15

```

Ser	Val	Ala	Ser	Phe	Ser	Tyr	Ala	Ala	Ser	Tyr	Thr	Pro	Pro	Ser	Thr
			20				25					30			
Ala	Val	Ser	Lys	Ile	Asn	Ser	Tyr	Arg	Gly	Tyr	Ser	Glu	Leu	Thr	Ser
		35					40					45			
Ala	Ala	Ser	Gly	Met	Asp	Ile	Asp	Gln	Tyr	Thr	Tyr	Asn	Met	Thr	Thr
		50				55					60				
Trp	Gln	Ile	Ala	Asn	Gly	Gly	Phe	Tyr	Lys	Ala	Met	Ala	Asp	Lys	Tyr
65				70					75					80	
Lys	Ser	Ala	Tyr	Gly	Gly	Gln	Lys	Ser	Glu	Trp	Gln	Ala	Lys	Gly	
			85				90						95		
Gly	Gly	Asp	Leu	Gly	Thr	Ile	Asp	Asn	Asn	Ala	Thr	Ile	Gln	Glu	Met
			100				105					110			
Arg	Leu	Leu	Ala	Val	Arg	Tyr	Lys	Glu	Thr	Thr	Asn	Asn	Asn	Tyr	Lys
		115					120					125			
Ser	Ala	Phe	Lys	Thr	Ser	Phe	Asn	Lys	Ala	Val	Asn	Phe	Leu	Leu	Thr
		130				135					140				
Met	Gln	Arg	Ser	Lys	Gly	Gly	Leu	Pro	Gln	Val	Trp	Pro	Lys	Arg	Gly
145				150					155					160	
Asn	Tyr	Ser	Asp	Gln	Ile	Thr	Leu	Asn	Asp	Asn	Ala	Met	Ile	Arg	Ala
			165					170					175		
Met	Val	Thr	Met	Met	Asp	Ile	Ala	Asn	Lys	Thr	Ser	Pro	Phe	Asp	Ser
			180				185						190		
Asp	Ile	Ile	Asp	Asp	Ala	Thr	Arg	Ser	Lys	Met	Lys	Ser	Ala	Leu	Asp
		195				200						205			
Lys	Ala	Val	Asp	Tyr	Leu	Leu	Lys	Ala	Gln	Ile	Val	Asn	Asp	Gly	Lys
		210				215					220				
Val	Thr	Val	Trp	Cys	Ala	Gln	His	Asp	Thr	Asn	Ser	Leu	Ala	Pro	Val
225				230					235					240	
Gly	Ala	Arg	Ala	Tyr	Glu	Leu	Pro	Ser	Lys	Ser	Gly	Asn	Glu	Ser	Met
			245						250					255	
Gly	Val	Val	Trp	Phe	Leu	Met	Asn	Trp	Pro	Asp	Gln	Asn	Glu	Ala	Ile
			260				265						270		
Gln	Lys	Ala	Val	Lys	Gly	Ala	Ile	Ala	Trp	Tyr	Lys	Lys	Asn	Lys	Leu
		275				280						285			
Lys	Asp	Lys	Ala	Phe	Ser	Lys	Thr	Ala	Gly	Val	Val	Asp	Lys	Ala	Gly
		290				295					300				
Ser	Ser	Leu	Trp	Phe	Arg	Phe	Tyr	Glu	Val	Asn	Asn	Asp	Asn	Tyr	Phe
305				310					315					320	
Phe	Cys	Asp	Arg	Asp	Gly	Ala	Ser	Thr	Lys	Thr	Gln	Asp	Phe	Met	Lys
			325						330					335	
Ile	Ser	Glu	Glu	Arg	Arg	Lys	Gly	Tyr	Gln	Trp	Ala	Gly	Asp	Tyr	Gly
			340				345						350		
Ser	Ala	Ile	Leu	Gly	Thr	Glu	Asn	Ala	Tyr	Leu	Glu	Ala	Leu	Ala	Lys
		355					360					365			
Met	Asp	Asp													

				485					490					495			
Phe	Thr	Ser	Leu	Ser	Lys	Asp	Gly	Met	Ala	Asn	Ile	Asp	Tyr	Ile	Gly		
			500					505					510				
Trp	Met	Asn	Asp	Asp	Leu	Lys	Val	Gly	Glu	Val	Glu	Val	Pro	Arg	Ser		
		515					520					525					
Ser	Ile	Glu	Ala	Ile	Arg	Ala	Ile	Arg	Lys	Ala	Gln	Gln	Asp	Asn	Arg		
	530					535					540						
Tyr	Phe	Val	Asp	Phe	Gly	Gly	Asn	Asn	Asn	Ser	Ala	Gly	Ala	Tyr	Phe		
545					550					555					560		
Lys	Arg	Gly	Ile	Asn	Thr	Phe	Arg	Val	Asn	Gly	Lys	Met	Arg				
				565					570								

<210> 119
 <211> 1848
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 119

gtgtcatggc	aggaatccgg	tgcggctatc	accaacgcct	ggaatgcaac	gctcagtgge	60
tcaaaccctt	acacagccgt	atccgctggt	tggaaatggca	cacttgcccc	caatgcatcg	120
gccacttttg	gtttccaggc	aaacggttct	gccgggtgcac	ctaaagtga	tggcagcttg	180
tgcggcacca	acacttcac	aacaccggca	tccagcagtg	ttgccagctc	ggttaaatca	240
agcgcgcccg	tatcgctccag	cagcagatca	tccagttcaa	tcgctatcac	tagcagctct	300
ttagcgagaa	gttctattgc	ctccagcagc	tcactagtta	gtagctccag	agcgagcagt	360
agtgcgcaa	gcgttttctc	ttttacgata	caggaagagc	aagcgggctt	ctgtcgtgtt	420
gatggcattg	cgacagaaa	caccaacacc	ggttttaccg	gcaatggcta	caccaatgcg	480
aacaacgcgc	aaggcgagc	gattgaatgg	gcagtcagcg	cacctagcag	tggccgttat	540
acagtagcct	tccgcttcgc	caatggcggc	acagcagcgc	gcaacggctc	gttggttaac	600
aatggcggtg	gcaatggtaa	ttacactgtg	gagttaccgc	tgaccggcgc	atgggcaacc	660
tggcaaattg	ccagcgtgga	aattgattta	gtgcaaggca	ataatatttt	aaaactctcg	720
gcgttaaccg	ctgacggttt	ggccaatata	gactcattaa	aaatagacgg	cgcgcaaacc	780
aaagcaggta	cttgacgac	tacatcaagc	agcagcgttg	ccagcagctc	gtcgtccgtt	840
aaatccagcg	caagttcttc	ttcgagttca	tccaccgctg	caaaaatact	gacattagac	900
ggtaaccggg	ccgccagctg	gttcaacaaa	tccaggacca	agtgggaatag	cagccgcgcc	960
gatatttgtg	tgtcttacca	gcaatccaac	ggcgggttgg	caaaaaacct	ggattacaac	1020
tcagtgagcg	caggcaatgg	cgggagcgac	agcggcacca	tcgacaatgg	tgcaaccatt	1080
accgaaatgg	tttacctcgc	tgaaatttat	aaaaacggcg	gcaacaccaa	atatcgcgat	1140
gcagtgcgca	gagcagcaaa	cttttttagtg	agctcgcaat	acagcacagg	cgccttgcca	1200
caatttttat	cgttgaaagg	cggctatgcg	gatcatgcga	cctttaacga	taacggcatg	1260
gcgtacgcgt	tgacggtatt	ggatttcgca	gtaaacaac	gcgcaccgtt	tgataacgac	1320
attttctctg	attctgatcg	ggcgaaattc	aaaaccgctg	ttgccaaagg	tgtggattac	1380
attttaaaag	cgcagtgga	acaaaatgga	aaactcactg	catggtgtgc	acaacacggt	1440
gctacggatt	accaaccgaa	aaaagcgcg	gcttatgaat	tggaatcatt	gagtggtagc	1500
gagtcggctg	gcattctcgc	cttcttgatg	acccaaccac	aaaccgcgca	aatcgaagcg	1560
gcgggtcaagg	cgggtgtcaa	ctggttcgcc	agtccaaata	cttatttggc	taactacact	1620
tacgattcat	caaaagcgtc	taccaaccgc	atttgttata	aatccggaag	cagaatgtgg	1680
tatcgcttct	atgacctgaa	caccaaccgt	ggtttcttta	gtgatcgcca	tggcagcaaa	1740
ttctatgata	tcacccaaat	gtcagaagag	cgtcgcaccg	gttatagctg	gggtggctct	1800
tacggtgaat	ctattatttc	cttcgcgcaa	aaagtgggtt	atctgtaa		1848

<210> 120
 <211> 615
 <212> PRT
 <213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> BINDING

<222> (1) ... (61)

<223> Carbohydrate binding module

<221> BINDING

 $\langle 222 \rangle \quad (134) \dots (257)$

<223> Carbohydrate binding module

<221> DOMAIN

$\langle 222 \rangle \quad (258) \dots (615)$

<223> Catalytic domain

<400> 120

Met 1	Ser	Trp	Gln	Glu 5	Ser	Gly	Ala	Ala	Ile 10	Thr	Asn	Ala	Trp	Asn 15	Ala
Thr	Leu	Ser	Gly 20	Ser	Asn	Pro	Tyr	Thr	Ala 25	Val	Ser	Ala	Gly 30	Trp	Asn
Gly	Thr	Leu 35	Ala	Pro	Asn	Ala	Ser 40	Ala	Thr	Phe	Gly	Phe 45	Gln	Ala	Asn
Gly	Ser	Ala	Gly	Ala	Pro	Lys 55	Val	Asn	Gly	Ser	Leu 60	Cys	Gly	Thr	Asn
Thr 65	Ser	Ser	Thr	Pro	Ala 70	Ser	Ser	Ser	Val	Ala 75	Ser	Ser	Val	Lys	Ser 80
Ser	Ala	Pro	Val	Ser 85	Ser	Ser	Ser	Arg	Ser 90	Ser	Ser	Ser	Ile	Ala 95	Ile
Thr	Ser	Ser	Ser 100	Leu	Ala	Arg	Ser	Ser	Ile 105	Ala	Ser	Ser	Ser	Ser	Leu
Val	Ser	Ser	Ser 115	Arg	Ala	Ser	Ser 120	Ser	Ala	Pro	Ser	Val	Phe	Ser	Phe
Thr	Ile	Gln	Glu 130	Glu	Gln	Ala 135	Gly	Phe	Cys	Arg	Val 140	Asp	Gly	Ile	Ala
Thr 145	Glu	Ser	Thr	Asn 150	Thr	Gly	Phe	Thr	Gly	Asn 155	Gly	Tyr	Thr	Asn	Ala 160
Asn	Asn	Ala	Gln	Gly 165	Ala	Ala	Ile	Glu	Trp 170	Ala	Val	Ser	Ala	Pro 175	Ser
Ser	Gly	Arg	Tyr 180	Thr	Val	Ala	Phe	Arg 185	Phe	Ala	Asn	Gly	Gly 190	Thr	Ala
Ala	Arg	Asn 195	Gly	Ser	Leu	Leu	Ile 200	Asn	Gly	Gly	Ser	Asn 205	Gly	Asn	Tyr
Thr	Val	Glu	Leu 210	Pro	Leu	Thr 215	Gly	Ala	Trp	Ala	Thr 220	Trp	Gln	Ile	Ala
Ser 225	Val	Glu	Ile	Asp 230	Leu	Val	Gln	Gly	Asn	Asn 235	Ile	Leu	Lys	Leu	Ser 240
Ala	Leu	Thr	Ala	Asp 245	Gly	Leu	Ala	Asn	Ile 250	Asp	Ser	Leu	Lys	Ile 255	Asp
Gly	Ala	Gln	Thr 260	Lys	Ala	Gly	Thr	Cys 265	Ser	Thr	Thr	Ser	Ser	Ser	Ser
Val	Ala	Ser 275	Ser	Ser	Ser	Ser	Val 280	Lys	Ser	Ser	Ala	Ser	Ser	Ser	Ser
Ser	Ser	Ser 290	Thr	Ala	Ala	Lys 295	Ile	Leu	Thr	Leu	Asp 300	Gly	Asn	Pro	Ala
Ala 305	Ser	Trp	Phe	Asn 310	Lys	Ser	Arg	Thr	Lys	Trp 315	Asn	Ser	Ser	Arg	Ala 320
Asp	Ile	Val	Leu	Ser 325	Tyr	Gln	Gln	Ser	Asn 330	Gly	Gly	Trp	Pro	Lys 335	Asn
Leu	Asp	Tyr	Asn 340	Ser	Val	Ser	Ala	Gly 345	Asn	Gly	Gly	Ser	Asp 350	Ser	Gly

Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu
 355 360 365
 Ile Tyr Lys Asn Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg
 370 375 380
 Ala Ala Asn Phe Leu Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro
 385 390 395 400
 Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe Asn
 405 410 415
 Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val Asn
 420 425 430
 Lys Arg Ala Pro Phe Asp Asn Asp Ile Phe Ser Asp Ser Asp Arg Ala
 435 440 445
 Lys Phe Lys Thr Ala Val Ala Lys Gly Val Asp Tyr Ile Leu Lys Ala
 450 455 460
 Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His Gly
 465 470 475 480
 Ala Thr Asp Tyr Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu Glu Ser
 485 490 495
 Leu Ser Gly Ser Glu Ser Val Gly Ile Leu Ala Phe Leu Met Thr Gln
 500 505 510
 Pro Gln Thr Ala Gln Ile Glu Ala Val Lys Ala Gly Val Asn Trp
 515 520 525
 Phe Ala Ser Pro Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser Ser
 530 535 540
 Lys Ala Ser Thr Asn Pro Ile Val Tyr Lys Ser Gly Ser Arg Met Trp
 545 550 555 560
 Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp Arg
 565 570 575
 Asp Gly Ser Lys Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg
 580 585 590
 Thr Gly Tyr Ser Trp Gly Gly Ser Tyr Gly Glu Ser Ile Ile Ser Phe
 595 600 605
 Ala Gln Lys Val Gly Tyr Leu
 610 615

<210> 121
 <211> 1047
 <212> DNA
 <213> Bacteria

<400> 121
 atgatgagat caagcatcgt caagctagtt gctttcagtg ttgtgggttat gttatggctc 60
 ggtgtatcct ttcaaacggc agaagcgaat acgccaaatt tcaacttaca aggctttgcc 120
 acgttaaagt ggggaacaac tgggtggtgca ggtggagatg tagtgacggt tcgtacaggg 180
 aatgaattaa taaacgcttt gaagtcctaa aaccctaata gtccgttaac aatttatgta 240
 aacggtacga taacacctag taatacgtct gatagtaaga tcgatattaa ggatgtttcc 300
 aatgtatcga ttttaggggt tggtaacaaat ggacgattaa atgggatcgg tattaagta 360
 tggcgagcga ataatatcat cattcgcaac ttgacgatcc atgaagtcca tacaggtgat 420
 aaagatgcga ttagcattga agggccctct cggaacattt ggattgacca taacgagctt 480
 tatgccagct tgaacgttca taaagaccac tatgacggct tgtttgacgt aaagcgcgat 540
 gcttacaata ttaccttctc ttggaattat gtccatgatg gctggaaagc gatgctcatg 600
 gggaactctg atagtataa ctacgaccga aacataacat tccaccataa ctacttcaaa 660
 aacttaaaact ctgcggtacc tgcgtaccgt tttggaaagg cgacttgtt tagcaattac 720
 tttgagaaca ttttagaaac aggcattaat tcacggatgg gagcggaat gctcgttgaa 780
 cataacgttt ttgagaatgc caccaaccgg ttaggattct ggcatagcag tcgaacagggt 840
 tattggaatg ttgccaataa ccgctatatc aatagcacgg gtagcatgcc gaccacttcc 900
 acgaccaatt atcgacctcc ttatccctat acggtcacac cagttggtga tgtgaaatcg 960
 gttgtcacac gttatgcggg agttggtgtc atccagccgt atgcaagaaa gccatccgag 1020
 cgattgctct ggtggctttt tgcataa 1047

<210> 122
 <211> 348
 <212> PRT
 <213> Bacteria

<220>

<221> SIGNAL
 <222> (1)...(29)

<221> DOMAIN
 <222> (30)...(348)
 <223> Catalytic domain

<400> 122
 Met Met Arg Ser Ser Ile Val Lys Leu Val Ala Phe Ser Val Val Val
 1 5 10 15
 Met Leu Trp Leu Gly Val Ser Phe Gln Thr Ala Glu Ala Asn Thr Pro
 20 25 30
 Asn Phe Asn Leu Gln Gly Phe Ala Thr Leu Asn Gly Gly Thr Thr Gly
 35 40 45
 Gly Ala Gly Gly Asp Val Val Thr Val Arg Thr Gly Asn Glu Leu Ile
 50 55 60
 Asn Ala Leu Lys Ser Lys Asn Pro Asn Arg Pro Leu Thr Ile Tyr Val
 65 70 75 80
 Asn Gly Thr Ile Thr Pro Ser Asn Thr Ser Asp Ser Lys Ile Asp Ile
 85 90 95
 Lys Asp Val Ser Asn Val Ser Ile Leu Gly Val Gly Thr Asn Gly Arg
 100 105 110
 Leu Asn Gly Ile Gly Ile Lys Val Trp Arg Ala Asn Asn Ile Ile Ile
 115 120 125
 Arg Asn Leu Thr Ile His Glu Val His Thr Gly Asp Lys Asp Ala Ile
 130 135 140
 Ser Ile Glu Gly Pro Ser Arg Asn Ile Trp Ile Asp His Asn Glu Leu
 145 150 155 160
 Tyr Ala Ser Leu Asn Val His Lys Asp His Tyr Asp Gly Leu Phe Asp
 165 170 175
 Val Lys Arg Asp Ala Tyr Asn Ile Thr Phe Ser Trp Asn Tyr Val His
 180 185 190
 Asp Gly Trp Lys Ala Met Leu Met Gly Asn Ser Asp Ser Asp Asn Tyr
 195 200 205
 Asp Arg Asn Ile Thr Phe His His Asn Tyr Phe Lys Asn Leu Asn Ser
 210 215 220
 Arg Val Pro Ala Tyr Arg Phe Gly Lys Ala His Leu Phe Ser Asn Tyr
 225 230 235 240
 Phe Glu Asn Ile Leu Glu Thr Gly Ile Asn Ser Arg Met Gly Ala Glu
 245 250 255
 Met Leu Val Glu His Asn Val Phe Glu Asn Ala Thr Asn Pro Leu Gly
 260 265 270
 Phe Trp His Ser Ser Arg Thr Gly Tyr Trp Asn Val Ala Asn Asn Arg
 275 280 285
 Tyr Ile Asn Ser Thr Gly Ser Met Pro Thr Thr Ser Thr Thr Asn Tyr
 290 295 300
 Arg Pro Pro Tyr Pro Tyr Thr Val Thr Pro Val Gly Asp Val Lys Ser
 305 310 315 320
 Val Val Thr Arg Tyr Ala Gly Val Gly Val Ile Gln Pro Tyr Ala Arg
 325 330 335
 Lys Pro Ser Glu Arg Leu Leu Trp Trp Leu Phe Ala

340

345

<210> 123
 <211> 1830
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<400> 123
 ttgagtctac ttagtgtaat gacccttttg cctgtaatgg caagtaacaa cgtagctccc 60
 tggggctggg ccacctgctc cgatgagtc ggcacagctt atactctgaa cggaggttgc 120
 ttttctgatg catcttccgt tactctgaaa gctcttggca atgaacaaac agatgacaaa 180
 caaatcaaac aggctatcgc tcagaaagac atcattatct tagatgggtc caatggcgat 240
 ttcatcctta atgaatacat caagatttcg accaaaaaca aaaccatcat tggatatcaac 300
 aacgcccgcc tgtgtacaaa gttctaccta accgctgatg atattacgta ccttaaagca 360
 caaggactgg agggactgag tagtacaaat caacatacag gaactctgcc tgatggcaca 420
 acagtgaacct gtgacgagcg tgcctttttc accaagaaag ccatcatgga actccaatat 480
 cagaaaacag gatcctatac cctacccaat aaatcaggtt tcttttattt agatgccgct 540
 tctgagaata tcatcatccg aaatatctcg ctgatagggc caggagccgt agatatagac 600
 ggagctgacc tgattaccaa tcagggttaag cacgtctgga ttgaccattg cacgtttgtg 660
 gactctcaag atggtgccc ggacagcaag gtatgcgact gggccaccta tacctataac 720
 cacttctact atacagaccg cagttactca catgcctaca cttgcggttg cggatgggtc 780
 agcaatcatg aaatggtgat tcacatgacc tttgcatgta atatctgggg agcaaaatgt 840
 atgcgtcgtc tgccgcaagc agatgactgt ttcatacacc ttgtgaacaa ctatcacaac 900
 tgtcctggca atagtgtcgg tatgaccatt aacagttaca gcaaagcatt ggttgagggt 960
 aactatgctg ctgcagggtg caacaagcca ttagatggca gtggggccaa ccgtaatgta 1020
 acagctaagg ataatagttt tgcaaactca caagccggtt ctggtgtgtc tgtgccatac 1080
 gactatacca agattgcagc cgccgacgtt ccagctacgc tgactggaac agagggtgca 1140
 ggcgccacat taggcaacga tgcaacatac attctgtcta ctattccaac tgtcgaccga 1200
 caagaaggcg aatcttcact ctactatttc attgatggcc tgggtgggaac taatagtga 1260
 ggctattcca ttatagagtt taatgatggc gcaacattgc tgctgaacaa taaagagaaa 1320
 gcatggtcta atggtagtgc aattcaactt ggtgacgata attatacgag tattaactt 1380
 tctaattggag cagaaaacat cttcacagca cctactggca aaaaagtaag tggattacc 1440
 ttctattctt atatcaatat aaaagaagaa aaactcgact tcaccaaata tccagaatat 1500
 ggtttccgca cctgtttctg gcagaaagtt gccaacctca cttattctgc gacttctgat 1560
 gacgtacaaa tcttgaaatc tcgtgatcca cagaatactg acgtggcatc attccatttc 1620
 actccaacaa atggttgaag tttcaaaaat tcaggtgaac agctttgttt cttaatgaaa 1680
 gtcacctata gtgatgaaag cacaggtatc tctgctatcc agaaaaaat gcctatcgat 1740
 ggcgttacct ataaccttca aggtatccgt atagataatc ccaccaaggg aatctatatt 1800
 cagaacggaa agaaaatcat tatcaataa 1830

<210> 124
 <211> 609
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample.

<221> SIGNAL
 <222> (1)...(21)

<221> DOMAIN
 <222> (22)...(390)
 <223> Catalytic domain

<400> 124

Leu	Ser	Leu	Leu	Ser	Val	Met	Thr	Leu	Leu	Pro	Val	Met	Ala	Ser	Asn
1				5				10						15	
Asn	Val	Ala	Pro	Trp	Gly	Trp	Ala	Thr	Cys	Ser	Asp	Glu	Ser	Ala	Thr
		20						25					30		
Ala	Tyr	Thr	Leu	Asn	Gly	Gly	Cys	Phe	Ser	Asp	Ala	Ser	Ser	Val	Thr
	35						40					45			
Leu	Lys	Ala	Leu	Gly	Asn	Glu	Gln	Thr	Asp	Asp	Lys	Gln	Ile	Lys	Gln
50					55						60				
Ala	Ile	Ala	Gln	Lys	Asp	Ile	Ile	Ile	Leu	Asp	Gly	Ser	Asn	Gly	Asp
65				70					75					80	
Phe	Ile	Leu	Asn	Glu	Tyr	Ile	Lys	Ile	Ser	Thr	Lys	Asn	Lys	Thr	Ile
			85						90					95	
Ile	Gly	Ile	Asn	Asn	Ala	Arg	Leu	Cys	Thr	Lys	Phe	Tyr	Leu	Thr	Ala
			100					105					110		
Asp	Asp	Ile	Thr	Tyr	Leu	Lys	Ala	Gln	Gly	Leu	Glu	Gly	Leu	Ser	Ser
		115					120					125			
Thr	Asn	Gln	His	Thr	Gly	Thr	Leu	Pro	Asp	Gly	Thr	Thr	Val	Thr	Cys
	130				135						140				
Asp	Glu	Arg	Ala	Phe	Phe	Thr	Lys	Lys	Ala	Ile	Met	Glu	Leu	Gln	Tyr
145				150					155					160	
Gln	Lys	Thr	Gly	Ser	Tyr	Thr	Leu	Pro	Asn	Lys	Ser	Gly	Ile	Phe	Tyr
			165						170					175	
Leu	Asp	Ala	Ala	Ser	Glu	Asn	Ile	Ile	Ile	Arg	Asn	Ile	Ser	Leu	Ile
		180						185					190		
Gly	Pro	Gly	Ala	Val	Asp	Ile	Asp	Gly	Ala	Asp	Leu	Ile	Thr	Asn	Gln
	195						200					205			
Gly	Lys	His	Val	Trp	Ile	Asp	His	Cys	Thr	Phe	Val	Asp	Ser	Gln	Asp
	210				215					220					
Gly	Ala	Leu	Asp	Ser	Lys	Val	Cys	Asp	Trp	Ala	Thr	Tyr	Thr	Tyr	Asn
225				230					235					240	
His	Phe	Tyr	Tyr	Thr	Asp	Arg	Ser	Tyr	Ser	His	Ala	Tyr	Thr	Cys	Gly
			245						250					255	
Cys	Gly	Trp	Val	Ser	Asn	His	Glu	Met	Val	Ile	His	Met	Thr	Phe	Ala
		260						265					270		
Cys	Asn	Ile	Trp	Gly	Ala	Lys	Cys	Met	Arg	Arg	Leu	Pro	Gln	Ala	Asp
		275					280					285			
Asp	Cys	Phe	Ile	His	Leu	Val	Asn	Asn	Tyr	His	Asn	Cys	Pro	Gly	Asn
	290					295					300				
Ser	Val	Gly	Met	Thr	Ile	Asn	Ser	Tyr	Ser	Lys	Ala	Leu	Val	Glu	Gly
305				310						315				320	
Asn	Tyr	Ala	Ala	Ala	Gly	Val	Asn	Lys	Pro	Leu	Asp	Gly	Ser	Gly	Ala
			325						330					335	
Asn	Arg	Asn	Val	Thr	Ala	Lys	Asp	Asn	Ser	Phe	Ala	Asn	Ser	Gln	Ala
		340						345					350		
Gly	Ser	Val	Val	Ser	Val	Pro	Tyr	Asp	Tyr	Thr	Lys	Ile	Ala	Ala	Ala
	355						360					365			
Asp	Val	Pro	Ala	Thr	Leu	Thr	Gly	Thr	Glu	Gly	Ala	Gly	Ala	Thr	Leu
	370					375					380				
Gly	Asn	Asp	Ala	Thr	Tyr	Ile	Leu	Ser	Thr	Ile	Pro	Thr	Val	Asp	Arg
385				390						395				400	
Gln	Glu	Gly	Glu	Ser	Ser	Leu	Tyr	Tyr	Phe	Ile	Asp	Gly	Leu	Val	Gly
			405						410					415	
Thr	Asn	Ser	Glu	Gly	Tyr	Ser	Ile	Ile	Glu	Phe	Asn	Asp	Gly	Ala	Thr
			420					425					430		
Leu	Leu	Leu	Asn	Asn	Lys	Glu	Lys	Ala	Trp	Ser	Asn	Gly	Ser	Ala	Ile
	435						440					445			
Gln	Leu	Gly	Asp	Asp	Asn	Tyr	Thr	Ser	Ile	Lys	Leu	Ser	Asn	Gly	Ala
	450					455					460				
Glu	Asn	Ile	Phe	Thr	Ala	Pro	Thr	Gly	Lys	Lys	Val	Ser	Gly	Ile	Thr

[illegible]

<210>	125
<211>	1170
<212>	DNA
<213>	Unknown

<220>
<223> Obtained from an environmental sample.

<400> 125							
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aatggcgatt	tcaactattag	tgctacaatg	agtttcagta	gcaaatacaa	caaaaccata		120
gttggtgtaa	ataatgctcg	cctatgcacc	aagttctatc	taaccgatga	aataaagact		180
gcgctcgatg	ctgctaattg	aaaatacaga	agttcaacca	gtggagggtg	tacactctca		240
aatgggaaat	cagtgctcaga	acaacgtgaa	taccttactc	gtcaaacaaat	tatcgatcta		300
actggcgatg	cttcgggaatc	gtgtcagaaa	gcgggcatct	ttagcttcag	tagttgtacc		360
aatatcatca	tgcgaaacct	cgttttgggt	ggccctggcc	catgcatgtg	aggtggcaac		420
gatttgcttt	cgctcactgg	ttctaagcat	ttttgggtcg	atcactgtga	gttaaccgat		480
ggtatagatg	gcaatttcga	tattaccaag	agtagcgatt	tcaatactgt	tacttggtgt		540
atattcaatt	ataccgatcg	tgcatacgac	cacatgaact	ccaatcttat	tggtagctcc		600
gatagcgaag	atgctgccta	tttgaacact	actatggcat	gcaatttttg	gggtacaag		660
tgcaatcagc	gaatgccaat	ggctcgtgct	ggtaatatct	accttgtgaa	caacttttac		720
gattgcgctg	gcaatagtg	ggctgttaac	cctcgtaaaa	attctgagtt	cttagtcgag		780
aactgctact	ttgccacggg	tgtgaagcca	ttctcgcaga	gtgggtgcgt	gggatacaac		840
tttattgatt	gctatacaga	agattcatac	acttttcagc	agagtggtag	agtgtctgtg		900
ccatacgttt	actctaagtt	tgatgtgcaa	ttagtaccgg	agcaactcaa	taaatatgct		960
ggcgcaacgc	ttactttctcc	gcttgtcata	ggtcgggaag	agggtgttgt	tactcctatt		1020
agtgtgtct	ctgttgatag	cgatgttgtg	ttggtcgaat	actattcgct	gactggtaat		1080
cgtgttaaca	cgctcaatat	aggcataaat	atcggttagaa	ctatttacgc	caacggcaaa		1140
gtaacccacac	aaaagqtttt	ggtgaaatag					1170

<210>	126
<211>	389
<212>	PRT
<213>	Unknown

<220>
<223> Obtained from an environmental sample.

<221> DOMAIN

<222> (24)...(325)

<223> Catalytic domain

<400> 126

```

Met Arg Ser Lys Ile Ile Ser Ala Ile Asn Asn Tyr Ser Val Ile Ile
 1           5           10           15
Leu Asp Gly Ser Asn Gly Asp Phe Thr Ile Ser Ala Thr Met Ser Phe
           20           25           30
Ser Ser Lys Ser Asn Lys Thr Ile Val Gly Val Asn Asn Ala Arg Leu
           35           40           45
Cys Thr Lys Phe Tyr Leu Thr Asp Glu Ile Lys Thr Ala Leu Asp Ala
           50           55           60
Ala Asn Val Lys Ser Ala Ser Ser Thr Ser Gly Gly Gly Thr Leu Ser
65           70           75           80
Asn Gly Lys Ser Val Ser Glu Gln Arg Glu Tyr Leu Thr Arg Gln Thr
           85           90           95
Ile Ile Asp Leu Thr Gly Asp Ala Ser Glu Ser Cys Gln Lys Ala Gly
           100          105          110
Ile Phe Ser Phe Ser Ser Cys Thr Asn Ile Ile Met Arg Asn Leu Val
           115          120          125
Leu Val Gly Pro Gly Pro Cys Asp Val Gly Gly Asn Asp Leu Leu Ser
           130          135          140
Leu Thr Gly Ser Lys His Phe Trp Val Asp His Cys Glu Leu Thr Asp
145           150          155          160
Gly Ile Asp Gly Asn Phe Asp Ile Thr Lys Ser Ser Asp Phe Asn Thr
           165          170          175
Val Thr Trp Cys Ile Phe Asn Tyr Thr Asp Arg Ala Tyr Asp His Met
           180          185          190
Asn Ser Asn Leu Ile Gly Ser Ser Asp Ser Glu Asp Ala Tyr Leu
           195          200          205
Asn Thr Thr Met Ala Cys Asn Ile Trp Gly Tyr Lys Cys Asn Gln Arg
           210          215          220
Met Pro Met Ala Arg Ala Gly Asn Ile His Leu Val Asn Asn Phe Tyr
225           230          235          240
Asp Cys Ala Gly Asn Ser Val Ala Val Asn Pro Arg Lys Asn Ser Glu
           245          250          255
Phe Leu Val Glu Asn Cys Tyr Phe Ala Thr Gly Val Lys Pro Phe Ser
           260          265          270
Gln Ser Gly Ala Leu Gly Tyr Asn Phe Ile Asp Cys Tyr Thr Glu Asp
           275          280          285
Ser Tyr Thr Phe Gln Gln Ser Gly Thr Val Ser Val Pro Tyr Val Tyr
           290          295          300
Ser Lys Phe Asp Val Gln Leu Val Pro Glu Gln Leu Asn Lys Tyr Ala
305           310          315          320
Gly Ala Thr Leu Thr Ser Pro Leu Val Ile Gly Arg Glu Glu Gly Val
           325          330          335
Val Thr Pro Ile Ser Ala Val Ser Val Asp Ser Asp Val Val Leu Val
           340          345          350
Glu Tyr Tyr Ser Leu Thr Gly Asn Arg Val Asn Thr Leu Asn Arg Gly
           355          360          365
Ile Asn Ile Val Arg Thr Ile Tyr Ala Asn Gly Lys Val Thr Thr Gln
           370          375          380
Lys Val Leu Val Lys
385

```

<210> 127

<211> 1449

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<400> 127

atgcaatatg	gcaaattagt	acgcttgctg	gcactgacaa	cagcgctggc	attcagcgcc	60
ctggcacagg	caaataacct	ggcaattaca	ggccccggag	ccggggctga	tggttccagc	120
aaagccagtg	gcagtagcta	cggcgatgta	aaagacgccg	atctgcaaag	ctactggcaa	180
ccgcctgcta	ataacggcca	aagagtgtcg	gttaagtggg	gcagcgctat	cagcggttaat	240
caggtaatat	tgcgtgaaca	gggcagtaat	gtaaccagct	ggcggctggt	aaataatgac	300
aacggcgag	tattggcaac	cggcaccagc	attggcagca	acagaacggt	taacttcagc	360
actgtaagca	cgaaaaaact	caatctggaa	atactaactg	ccagcggtgc	cccgcgcatt	420
gctgagtttg	aagttttatt	aaataccaat	ggcggcaacc	cgccaaatcc	tactgaccgc	480
gaaccaggcc	cggtaacttc	ttgcgcagcg	tctccacagg	gctatgcctc	gcttaacggt	540
ggcactaccg	gcggcagtg	cagcaacgcg	gtcacggtaa	cggtaagcac	cggcgctcaa	600
atggtagcgg	cgtacaaaa	ccgcgatcta	aaccggccgc	tcactatccg	ggtaaatggc	660
actatcacac	cgggtaattc	tggcgggtgc	agtaagtttg	acattaaaga	tatggataat	720
gtcagcatta	ttggtgtagg	caacaatgcg	ttgtttgacg	gtatcgggtat	taaaatctgg	780
cgggccaata	acgtttattat	ccgcaacctt	acaatgcgtt	atgttaacac	cggcgataaa	840
gacgctatta	ccattgaagg	ccggcgcggt	aatatctgga	ttgaccacaa	cgaaatctat	900
aacagcctga	atgtgggtaa	agattttttac	gacgagctta	taagcggtaa	aaaagacgta	960
gataacgtaa	ctatctctta	caactacctg	cacgacagct	ggaaaacctc	gctgtggggc	1020
agcagtgtat	ccgacaacta	caaccgccgt	attacctttc	accataacca	ctggcataag	1080
gtaaattcac	gcttgccact	gttccgtttt	ggccaggggc	atattttaca	taactattac	1140
aacgacattc	aggacaccgg	tattaacagc	cggatgggtg	cggtaattcg	tattgaaaac	1200
aatgtgtttg	aaaacgcgaa	aaacccgata	gtgtcgtttt	attccagcgg	ctacggttac	1260
tgggacaccc	gcggtaatat	ctttagcaat	attacctggc	aggaataccc	cagcgacggc	1320
attatcgccg	ggccaaatgt	acaaccacac	gcggtgctaa	acctgcccta	cagctttaac	1380
ctgttaccca	ccaaccaggt	aaaagcccac	gtactggcca	acgccggcgt	gaataaatgt	1440
agttttctaa						1449

<210> 128

<211> 482

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample.

<221> SIGNAL

<222> (1)...(24)

<221> DOMAIN

<222> (5)...(482)

<223> Catalytic domain

<400> 128

Met	Gln	Tyr	Gly	Lys	Leu	Val	Arg	Leu	Ser	Ala	Leu	Thr	Thr	Ala	Leu
1				5				10						15	
Ala	Phe	Ser	Ala	Leu	Ala	Gln	Ala	Asn	Asn	Leu	Ala	Ile	Thr	Gly	Pro
			20					25					30		
Gly	Ala	Gly	Ala	Asp	Gly	Ser	Ser	Lys	Ala	Ser	Gly	Ser	Ser	Tyr	Gly
			35					40				45			
Asp	Val	Lys	Asp	Ala	Asp	Leu	Gln	Ser	Tyr	Trp	Gln	Pro	Pro	Ala	Asn
			50			55					60				
Asn	Gly	Gln	Arg	Val	Ser	Val	Lys	Trp	Ser	Ser	Ala	Ile	Ser	Val	Asn
65					70				75					80	
Gln	Val	Ile	Leu	Arg	Glu	Gln	Gly	Ser	Asn	Val	Thr	Ser	Trp	Arg	Leu
				85				90						95	

Val	Asn	Asn	Asp	Asn	Gly	Ala	Val	Leu	Ala	Thr	Gly	Thr	Ser	Ile	Gly	100	105	110
Ser	Asn	Arg	Thr	Val	Asn	Phe	Ser	Thr	Val	Ser	Thr	Lys	Lys	Leu	Asn	115	120	125
Leu	Glu	Ile	Leu	Thr	Ala	Ser	Gly	Ala	Pro	Arg	Ile	Ala	Glu	Phe	Glu	130	135	140
Val	Tyr	Leu	Asn	Thr	Asn	Gly	Gly	Asn	Pro	Pro	Asn	Pro	Thr	Asp	Pro	145	150	155
Glu	Pro	Gly	Pro	Val	Thr	Ser	Cys	Ala	Ala	Ser	Pro	Gln	Gly	Tyr	Ala	165	170	175
Ser	Leu	Asn	Gly	Gly	Thr	Thr	Gly	Gly	Ser	Gly	Ser	Asn	Ala	Val	Thr	180	185	190
Val	Thr	Val	Ser	Thr	Gly	Ala	Gln	Met	Val	Ser	Ala	Leu	Gln	Asn	Arg	195	200	205
Asp	Leu	Asn	Arg	Pro	Leu	Thr	Ile	Arg	Val	Asn	Gly	Thr	Ile	Thr	Pro	210	215	220
Gly	Asn	Ser	Gly	Gly	Val	Ser	Lys	Phe	Asp	Ile	Lys	Asp	Met	Asp	Asn	225	230	235
Val	Ser	Ile	Ile	Gly	Val	Gly	Asn	Asn	Ala	Leu	Phe	Asp	Gly	Ile	Gly	245	250	255
Ile	Lys	Ile	Trp	Arg	Ala	Asn	Asn	Val	Ile	Ile	Arg	Asn	Leu	Thr	Met	260	265	270
Arg	Tyr	Val	Asn	Thr	Gly	Asp	Lys	Asp	Ala	Ile	Thr	Ile	Glu	Gly	Pro	275	280	285
Ala	Arg	Asn	Ile	Trp	Ile	Asp	His	Asn	Glu	Ile	Tyr	Asn	Ser	Leu	Asn	290	295	300
Val	Gly	Lys	Asp	Phe	Tyr	Asp	Glu	Leu	Ile	Ser	Gly	Lys	Lys	Asp	Val	305	310	315
Asp	Asn	Val	Thr	Ile	Ser	Tyr	Asn	Tyr	Leu	His	Asp	Ser	Trp	Lys	Thr	325	330	335
Ser	Leu	Trp	Gly	Ser	Ser	Asp	Ser	Asp	Asn	Tyr	Asn	Arg	Arg	Ile	Thr	340	345	350
Phe	His	His	Asn	His	Trp	His	Lys	Val	Asn	Ser	Arg	Leu	Pro	Leu	Phe	355	360	365
Arg	Phe	Gly	Gln	Gly	His	Ile	Tyr	Asn	Asn	Tyr	Tyr	Asn	Asp	Ile	Gln	370	375	380
Asp	Thr	Gly	Ile	Asn	Ser	Arg	Met	Gly	Ala	Val	Ile	Arg	Ile	Glu	Asn	385	390	395
Asn	Val	Phe	Glu	Asn	Ala	Lys	Asn	Pro	Ile	Val	Ser	Phe	Tyr	Ser	Ser	405	410	415
Gly	Tyr	Gly	Tyr	Trp	Asp	Thr	Arg	Gly	Asn	Ser	Phe	Ser	Asn	Ile	Thr	420	425	430
Trp	Gln	Glu	Tyr	Pro	Ser	Asp	Gly	Ile	Ile	Ala	Gly	Pro	Asn	Val	Gln	435	440	445
Pro	Thr	Ala	Val	Leu	Asn	Leu	Pro	Tyr	Ser	Phe	Asn	Leu	Leu	Pro	Thr	450	455	460
Asn	Gln	Val	Lys	Ala	His	Val	Leu	Ala	Asn	Ala	Gly	Val	Asn	Lys	Cys	465	470	475
Ser	Phe																	480

<210> 129

<211> 1173

<212> DNA

<213> Bacillus halodurans ATCC 27557

<220>

<400> 129

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atgagttcga aaatcaaaaa tgctatcaat aactatagtg ttattattct cgatggctcg      60
aatggcgatt ttacagtcaa tgctacaatg agtttcagtg gcaagtccaa taaaactatt      120
gtgggtgtga acaatgctcg cctatgcacc aaattctaca ttacgcccga gataaaagaa      180
gccctcgatg ctgccgatgt gaaatctaag agctcaagta gtggcactgg tggaaactctt      240
tctaattggtg cgtcggtcag tgaggctcgc gaattggcta ctcgtcaaac gttgattgat      300
tatctcggcg atagctcaga atcgtatcag aaagctggta tctttggctt tagcaactgc      360
actaatatta ttatgcgcaa cattgttttc gttggccctg gtccatgcga tgtagggtggc      420
aacgacttgc tttcgtctcg tggttcgaag catttctggg tcgaccactg cgagtttacc      480
gatggcatcg atggcaactt cgacatcacc aagagtagcg acttcaacac cgtttcgtgg      540
tgcactttca gctataccga ccgcgcatac gaccacatga attccaacct tattggtagc      600
tccgattcag agaatgcggc ttaccttaat actactatgg cttccaacgt ctggggcaat      660
aagtgcaatc agcgtatgcc tatggctcgt gccggtaata ttcacctcgt aaataattat      720
tacaactgcc ctggcaatag cgtggctgtg aatcctcgca aaaactcaga atttttggtg      780
gagaattgct atttcgcaag tggcgtaaag cttttctcgc agagcggcgc tcttagctat      840
ctatttatcg attgctacac cgaagatact tacaccttcc agaaatctgg ctctactacg      900
gtgccataca catatagcaa attcgaatgc cagcttggtc ccgagcaact caccacaattc      960
gctggcgcaa cattgacttc gccgcttggt attggtaggg aatctgagaa tgttacacca     1020
gtctcagtcg ttgctgcaaa tagcgatgtc atatctgtag aatactattc gctcactggc     1080
aagcgcacat gcgaaccaac taaaggcatc aatatcgta gaactattta tactaacggc     1140
aacgtgacca cacaaaaggt cttggtgaaa taa                                     1173

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<210> 130

<211> 390

<212> PRT

<213> Bacillus halodurans ATCC 27557

<220>

<221> DOMAIN

<222> (38)...(326)

<223> Catalytic domain

<400> 130

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Met Ser Ser Lys Ile Lys Asn Ala Ile Asn Asn Tyr Ser Val Ile Ile
 1           5           10           15
Leu Asp Gly Ser Asn Gly Asp Phe Thr Val Asn Ala Thr Met Ser Phe
          20           25           30
Ser Gly Lys Ser Asn Lys Thr Ile Val Gly Val Asn Asn Ala Arg Leu
          35           40           45
Cys Thr Lys Phe Tyr Ile Thr Pro Glu Ile Lys Glu Ala Leu Asp Ala
          50           55           60
Ala Asp Val Lys Ser Lys Ser Ser Ser Ser Gly Thr Gly Gly Thr Leu
65           70           75           80
Ser Asn Gly Thr Ser Val Ser Glu Ala Arg Glu Leu Ala Thr Arg Gln
          85           90           95
Thr Leu Ile Asp Tyr Leu Gly Asp Ser Ser Glu Ser Tyr Gln Lys Ala
          100          105          110
Gly Ile Phe Gly Phe Ser Asn Cys Thr Asn Ile Ile Met Arg Asn Ile
          115          120          125
Val Phe Val Gly Pro Gly Pro Cys Asp Val Gly Gly Asn Asp Leu Leu
          130          135          140
Ser Leu Val Gly Ser Lys His Phe Trp Val Asp His Cys Glu Phe Thr
145          150          155          160
Asp Gly Ile Asp Gly Asn Phe Asp Ile Thr Lys Ser Ser Asp Phe Asn
          165          170          175
Thr Val Ser Trp Cys Thr Phe Ser Tyr Thr Asp Arg Ala Tyr Asp His
          180          185          190
Met Asn Ser Asn Leu Ile Gly Ser Ser Asp Ser Glu Asn Ala Ala Tyr
          195          200          205

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Leu Asn Thr Thr Met Ala Ser Asn Val Trp Gly Asn Lys Cys Asn Gln
 210 215 220
 Arg Met Pro Met Ala Arg Ala Gly Asn Ile His Leu Val Asn Asn Tyr
 225 230 235 240
 Tyr Asn Cys Pro Gly Asn Ser Val Ala Val Asn Pro Arg Lys Asn Ser
 245 250 255
 Glu Phe Leu Val Glu Asn Cys Tyr Phe Ala Ser Gly Val Lys Pro Phe
 260 265 270
 Ser Gln Ser Gly Ala Leu Ser Tyr Leu Phe Ile Asp Cys Tyr Thr Glu
 275 280 285
 Asp Thr Tyr Thr Phe Gln Lys Ser Gly Ser Thr Thr Val Pro Tyr Thr
 290 295 300
 Tyr Ser Lys Phe Asp Ala Gln Leu Val Pro Glu Gln Leu Thr Gln Phe
 305 310 315 320
 Ala Gly Ala Thr Leu Thr Ser Pro Leu Val Ile Gly Arg Glu Ser Glu
 325 330 335
 Asn Val Thr Pro Val Ser Val Ile Ala Ala Asn Ser Asp Val Ile Ser
 340 345 350
 Val Glu Tyr Tyr Ser Leu Thr Gly Lys Arg Ile Ser Glu Pro Thr Lys
 355 360 365
 Gly Ile Asn Ile Val Arg Thr Ile Tyr Thr Asn Gly Asn Val Thr Thr
 370 375 380
 Gln Lys Val Leu Val Lys
 385 390

<210> 131
 <211> 972
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 131
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 accaagtggga atagcagccg cgccgatatt gtgttgtctt accagcaatc caacggcggt 120
 tggcaaaaaa acctggatta caactcagtg agcgcaggca atggcgggag cgacagcggc 180
 accatcgaca atggtgcaac cattaccgaa atggtttacc tcgctgaaat ttataaaaac 240
 ggcgggcaaca ccaaatatcg cgatgcagtg cgcagagcag caaacttttt agtgagctcg 300
 caatacacgca caggcgccctt gccacaattt tatccgttga aaggcgggcta tgcggatcat 360
 gcgaccttta acgataacgg catggcggtac gcgttgacgg tattggattt cgcagtaaac 420
 aaacgcgcac cgtttgataa cgacattttc tctgattctg atcgggcgaa attcaaaacc 480
 gctgttgcca aagggtgtgga ttacatttta aaagcgcagt ggaaacaaaa tggaaaactc 540
 actgcatggt gtgcacaaca cgggtgctacg gattaccaac cgaaaaaagc gcgcgcttat 600
 gaattggaat cattgagtgg tagcagagtcg gtcggcattc tcgccttctt gatgacccaa 660
 ccacaaaccg cgcaaatcga agcggcggtc aaggcgggtg tcaactggtt cgccagtcca 720
 aatacttatt tggctaacta cacttacgat tcatcaaaag cgtctaccaa cccgattgtg 780
 tataaatccg gaagcagaat gtggtatcgc ttctatgacc tgaacaccaa ccgtggtttc 840
 tttagtgatc gcgatggcag caaattctat gatatcacc aaatgtcaga agagcgtcgc 900
 accggttata gctgggggtg ctcttacggt gaatctatta tttccttcgc gcaaaaagtg 960
 gggttatctgt ag 972

<210> 132
 <211> 323
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 132

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Met Ala Lys Ile Leu Thr Leu Asp Gly Asn Pro Ala Ala Ser Trp Phe
 1          5          10          15
Asn Lys Ser Arg Thr Lys Trp Asn Ser Ser Arg Ala Asp Ile Val Leu
 20          25          30
Ser Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys Asn Leu Asp Tyr Asn
 35          40          45
Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser Gly Thr Ile Asp Asn
 50          55          60
Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu Ile Tyr Lys Asn
 65          70          75          80
Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg Ala Ala Asn Phe
 85          90          95
Leu Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro Gln Phe Tyr Pro
100          105          110
Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe Asn Asp Asn Gly Met
115          120          125
Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val Asn Lys Arg Ala Pro
130          135          140
Phe Asp Asn Asp Ile Phe Ser Asp Ser Asp Arg Ala Lys Phe Lys Thr
145          150          155          160
Ala Val Ala Lys Gly Val Asp Tyr Ile Leu Lys Ala Gln Trp Lys Gln
165          170          175
Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His Gly Ala Thr Asp Tyr
180          185          190
Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu Glu Ser Leu Ser Gly Ser
195          200          205
Glu Ser Val Gly Ile Leu Ala Phe Leu Met Thr Gln Pro Gln Thr Ala
210          215          220
Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn Trp Phe Ala Ser Pro
225          230          235          240
Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser Ser Lys Ala Ser Thr
245          250          255
Asn Pro Ile Val Tyr Lys Ser Gly Ser Arg Met Trp Tyr Arg Phe Tyr
260          265          270
Asp Leu Asn Thr Asn Arg Gly Phe Ser Asp Arg Asp Gly Ser Lys
275          280          285
Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg Thr Gly Tyr Ser
290          295          300
Trp Gly Gly Ser Tyr Gly Glu Ser Ile Ile Ser Phe Ala Gln Lys Val
305          310          315          320
Gly Tyr Leu

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<210> 133

<211> 972

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated polynucleotide

<400> 133

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atggcaaaaa tactgacatt agacggtaac ccggccgccca gctggttcaa caaatccagg      60
accaaagtgga atagcagccg cgccgatatt gtgtgtgttt accagcaatc caacggcggt      120
tggccaaaaa acctggatta caactcagtg agcgcaggca atggcgggag cgacagcggc      180
accatcgaca atggtgcaac cattaccgaa atggtttacc tcgctgaaat ttataaaaac      240
ggcggcaaca ccaaatatcg cgatgcagtg cgcagagcag caaacttttt agtgagctcg      300

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caatacagca caggcgccctt gccacaattt tatccggttga aaggcgggcta tcatgatcat 360
gcgaccttta acgataacgg catggcggtac gcgttgacgg tattggattt cgcagtaaac 420
aaacgcgcac cgtttgataa cgacattttc tctgattctg atcgggcgaa attcaaaacc 480
gctggttgcca aaggtgtgga ttacatttta aaagcgcagt ggaaacaaaa tggaaaactc 540
actgcatggt gtgcacaaca cgggtgctttg gattaccaac cgaaaaaagg tcgcgcttat 600
gaattggaat cattgagtggt taaggagtcg gtcggcattc tcgccttctt gatgacccaa 660
ccacaaaccg cgcaaatacg agcggcggtc aaggcgggtg tcaactgggt cgccagtcca 720
aatacttatt tggctaacta cacttacgat tcatcaaaag cgtctaccaa cccgattgtg 780
tataaaaaagg gaagcagaat gtggtatcgc ttctatgacc tgtataccaa ccgtgggttc 840
tttagtgatc gcgatggcag caaattctat gatatcacc aaatgtcaga agagcgtcgc 900
accggttata gctgggggtg ctcttggggg gaagttatta tttccttcgc gcaaaaagtg 960
ggttatctgt ag 972

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<210> 134

<211> 323

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetically generated polypeptide

<400> 134

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Met Ala Lys Ile Leu Thr Leu Asp Gly Asn Pro Ala Ala Ser Trp Phe
 1           5           10           15
Asn Lys Ser Arg Thr Lys Trp Asn Ser Ser Arg Ala Asp Ile Val Leu
      20           25           30
Ser Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys Asn Leu Asp Tyr Asn
      35           40           45
Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser Gly Thr Ile Asp Asn
      50           55           60
Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu Ile Tyr Lys Asn
      65           70           75           80
Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg Ala Ala Asn Phe
      85           90           95
Leu Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro Gln Phe Tyr Pro
      100          105          110
Leu Lys Gly Tyr His Asp His Ala Thr Phe Asn Asp Asn Gly Met
      115          120          125
Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val Asn Lys Arg Ala Pro
      130          135          140
Phe Asp Asn Asp Ile Phe Ser Asp Ser Asp Arg Ala Lys Phe Lys Thr
      145          150          155          160
Ala Val Ala Lys Gly Val Asp Tyr Ile Leu Lys Ala Gln Trp Lys Gln
      165          170          175
Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His Gly Ala Leu Asp Tyr
      180          185          190
Gln Pro Lys Lys Gly Arg Ala Tyr Glu Leu Glu Ser Leu Ser Gly Lys
      195          200          205
Glu Ser Val Gly Ile Leu Ala Phe Leu Met Thr Gln Pro Gln Thr Ala
      210          215          220
Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn Trp Phe Ala Ser Pro
      225          230          235          240
Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser Ser Lys Ala Ser Thr
      245          250          255
Asn Pro Ile Val Tyr Lys Lys Gly Ser Arg Met Trp Tyr Arg Phe Tyr
      260          265          270
Asp Leu Tyr Thr Asn Arg Gly Phe Phe Ser Asp Arg Asp Gly Ser Lys
      275          280          285
Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg Thr Gly Tyr Ser

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PCT/0504/10229

	290					295						300					
Trp	Gly	Gly	Ser	Trp	Gly	Glu	Val	Ile	Ile	Ser	Phe	Ala	Gln	Lys	Val		
305					310					315						320	
Gly	Tyr	Leu															